

GenCore version 5.1.6
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OM protein - protein search, using 6w model

Run on: December 12, 2005, 08:17:24 ; Search time 189 Seconds

(without alignment)
855.510 Million cell updates/sec

Title: US-10-681-878A-6

Perfect score: 1915

Sequence: 1 MGSTSETMSPSEAAAAEE.....PRVNSCAVNTWTFLEPKI 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 433378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

- A_Geneseqp21:*
- 1: geneeqp19808:*
 - 2: geneeqp19808:*
 - 3: geneeqp20008:*
 - 4: geneeqp20018:*
 - 5: geneeqp20028:*
 - 6: geneeqp20038:*
 - 7: geneeqp20048:*
 - 8: geneeqp20048:*
 - 9: geneeqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1915	100.0	368	2	AAI23342 A blifunct
2	1915	100.0	368	3	AAI19695 Sweetgum
3	1915	100.0	368	4	AAE05829 L. styrac
4	1915	100.0	368	9	ADZ14866 Syringyl
5	1595.5	83.3	365	2	AAV01133 Aspen bis
6	1595.5	83.3	365	5	AAU80015 S-hydroxy
7	1595.5	83.3	365	7	ADD93900 Quaking a
8	1589.5	83.0	365	6	AAO30114 Strawberry
9	1578.5	82.4	364	2	AAW84132 Exemplary
10	1578.5	81.8	365	5	AAE16510 Soybean c
11	1566.5	81.8	365	7	AD129674 Soybean c
12	1566.5	81.8	365	8	ADJ96484 Soybean c
13	1566.5	81.8	365	8	AAE16517 Soybean c
14	1544.5	80.7	365	2	AAE16517 Soybean c
15	1544.5	80.7	365	4	AAE16517 Soybean c
16	1544.5	80.7	365	8	ADK39712 Medicago
17	1528	79.8	370	8	ADK39712 Alfalfa c
18	1493.5	78.0	364	2	AAE16517 Soybean c
19	1492	77.9	358	7	AD129688 Soybean c
20	1492	77.9	358	8	ADJ96498 Soybean c
21	1473.5	76.9	363	3	AAE16517 Soybean c
22	1473.5	76.9	363	3	AAE16517 Soybean c
23	1473.5	76.9	363	3	AAE16517 Soybean c
24	1473.5	76.9	363	5	AAE16517 Soybean c

25	1473.5	76.9	363	8	ADN73605	Adn73
26	1420.5	74.2	340	3	AAE16517	Adn73
27	1420.5	74.2	340	3	AAE16517	Adn73
28	1393.5	72.8	312	8	ADY07282	Ady07
29	1387	72.4	343	8	ADK39715	Adk39
30	1379.5	72.0	330	3	AAE16517	Adk39
31	1379.5	72.0	330	3	AAE16517	Adk39
32	1379.5	72.0	330	3	AAE16517	Adk39
33	1344	70.2	368	2	AAE16517	Adk39
34	1341	70.0	368	6	AAE16517	Adk39
35	1332.5	69.6	314	2	AAE16517	Adk39
36	1326.5	69.3	316	3	AAE16517	Adk39
37	1320.5	69.0	309	3	AAE16517	Adk39
38	1246	65.1	360	7	ADK39716	Adk39
39	1246	65.1	360	7	ADK39716	Adk39
40	1246	65.1	360	7	ADK39716	Adk39
41	1244	65.0	356	5	AAE16517	Adk39
42	1244	65.0	356	7	AD129676	Adk39
43	1244	65.0	356	8	ADJ96486	Adk39
44	1244	65.0	360	7	ADK39716	Adk39
45	1244	65.0	360	7	ADK39716	Adk39
46	1243	64.9	360	7	ADK39716	Adk39
47	1243	64.9	360	7	ADK39716	Adk39
48	1238	64.6	360	5	AAE16517	Adk39
49	1236	64.5	360	7	ADK39716	Adk39
50	1236	64.5	360	7	ADK39716	Adk39
51	1225.5	64.0	356	8	ADK39716	Adk39
52	1204.5	62.9	361	7	ADK39716	Adk39
53	1204.5	62.9	361	7	ADK39716	Adk39
54	1194	62.3	368	3	AAE16517	Adk39
55	1188.5	62.1	361	6	AAE16517	Adk39
56	1170	61.1	368	6	AAE16517	Adk39
57	1154	60.3	362	8	ADK39716	Adk39
58	1144.5	59.8	351	5	AAE16517	Adk39
59	1144.5	59.7	371	9	ADK39716	Adk39
60	1133	59.2	400	3	AAE16517	Adk39
61	1133	59.2	400	3	AAE16517	Adk39
62	1090.5	56.9	365	8	ADK39716	Adk39
63	1073	56.0	362	5	AAE16517	Adk39
64	1073	56.0	362	7	ADK39716	Adk39
65	1073	56.0	362	8	ADK39716	Adk39
66	1049.5	54.8	365	2	AAE16517	Adk39
67	1047	54.7	365	2	AAE16517	Adk39
68	1037	54.2	364	3	AAE16517	Adk39
69	988.5	51.6	354	5	AAE16517	Adk39
70	988.5	51.6	354	7	ADK39716	Adk39
71	988.5	51.6	354	8	ADK39716	Adk39
72	984	51.4	351	5	AAE16517	Adk39
73	964.5	50.4	264	3	AAE16517	Adk39
74	964.5	50.4	264	3	AAE16517	Adk39
75	964.5	50.4	264	7	ADK39716	Adk39
76	964.5	50.4	264	7	ADK39716	Adk39
77	957	50.0	351	5	AAE16517	Adk39
78	948.5	49.5	352	7	ADK39716	Adk39
79	947	49.5	305	5	AAE16517	Adk39
80	947	49.5	305	7	ADK39716	Adk39
81	947	49.5	305	8	ADK39716	Adk39
82	936	43.7	372	8	ADK39716	Adk39
83	836	43.7	372	8	ADK39716	Adk39
84	832	43.4	363	5	AAE16517	Adk39
85	831.5	43.4	381	5	AAE16517	Adk39
86	830.5	43.4	381	3	AAE16517	Adk39
87	830.5	43.4	381	5	AAE16517	Adk39
88	827.5	43.2	354	3	AAE16517	Adk39
89	822	42.9	318	8	ADK39716	Adk39
90	817.5	42.7	338	8	ADK39716	Adk39
91	811.5	42.4	352	5	AAE16517	Adk39
92	803.5	42.0	373	5	AAE16517	Adk39
93	803.5	42.0	373	8	ADK39716	Adk39
94	802	41.9	340	3	AAE16517	Adk39
95	798.5	41.7	273	3	AAE16517	Adk39
96	798.5	41.7	417	3	AAE16517	Adk39
97	794.5	41.5	346	3	AAE16517	Adk39

98	794.5	41.5	373	5	ABB91081	Abb91081 Herbicida
99	794.5	41.5	373	8	ADN74367	Adn74367 Thale cre
100	790.5	41.3	373	5	ABB91083	Abb91083 Herbicida

ALIGNMENTS

RESULT 1

AAV23342 standard; protein, 368 AA.

AAV23342;

01-SEP-1999 (first entry)

A bifunctional-O-methyl transferase involved in lignin production.

Bifunctional-O-methyl transferase; syringyl lignin; angiosperm;

loblolly pine; Pinus taeda; lignin; woody plant; paper manufacture;

delignification; pulp mill; gymnosperm.

Liquidambar styraciflua.

WO931243-A1.

16-DEC-1998; 98WO-US026784.

16-DEC-1997; 97US-00991677.

(INTO) INT PAPER CO.

Chiang VL, Carraway DT, Smeltzer RH;

WPI; 1999-405034/34.

N-PSDB; AAX81875.

New DNA sequences encoding angiosperm enzymes involved in biosynthesis of

syringyl lignin.

Example 1; Fig 2D-E; 83pp; English.

The present sequence represents a bifunctional-O-methyl transferase which

is involved in syringyl lignin production in an angiosperm. The sequences

are used to produce syringyl lignin in gymnosperms, especially the

loblolly pine (Pinus taeda). It is necessary to remove much of the lignin

from the fiber/lignin network of woody plants in paper manufacture.

Greater proportions of syringyl lignin result in a higher delignification

rate and hence a more efficient pulp mill operation

Sequence 368 AA;

Query Match 100.0%; Score 1915; DB 2; Length 368;

Best Local Similarity 100.0%; Pred. No. 4.8e-196;

Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGSTSETKMSPEBAABEAEAFVPMQLTSASVLPVMTLSAIELDVLEITMAKAGCAHIS 60

1 MOSTSETKMSPEBAABEAEAFVPMQLTSASVLPVMTLSAIELDVLEITMAKAGCAHIS 60

61 TSIDASKLPDKNPDAVMDRLMLRLASYSVLTCSRLTPDKGIRLVLGLAVCKFLTN 120

61 TSIDASKLPDKNPDAVMDRLMLRLASYSVLTCSRLTPDKGIRLVLGLAVCKFLTN 120

121 DDGVSIALSLNODVLMESWYHLTEAVLEGIPENKAYGNTAFEGHGTDRFTVFN 180

121 DDGVSIALSLNODVLMESWYHLTEAVLEGIPENKAYGNTAFEGHGTDRFTVFN 180

181 GMSNSTITMKILLETYYKGFEGISVVDVGGGTGAHLNMIINAKYPMIKINFDLPHVIEE 240

181 GMSNSTITMKILLETYYKGFEGISVVDVGGGTGAHLNMIINAKYPMIKINFDLPHVIEE 240

QY	241	APSYGVEHVGDMFVSYPKGDATFMKWTCHDWSDEHCLKPLKCYEALP.	3C 300
DB	241	APSYGVEHVGDMFVSYPKGDALFMKWTCHDWSDEHCLKPLKCYEALP.	3C 300

RESULT 2

AAV23342 standard; protein, 368 AA.

AAV23342;

05-FEB-2001 (first entry)

Sweetgum bifunctional O-methyltransferase.

Sweetgum; angiosperm; bifunctional O-methyltransferase; bi-

functional O-methyltransferase; loblolly pine; transgenic plant; lignin

pulping.

Liquidambar styraciflua.

WO200058489-A2.

05-OCT-2000.

24-MAR-2000; 2000WO-US008083.

26-MAR-1999; 99US-00277248.

(INTO) INT PAPER CO.

Chiang VL, Carraway DT;

WPI; 2000-647240/62.

N-PSDB; AAA86683.

Use of angiosperm coniferyl aldehyde 5-hydroxylase which cat

alyzes the hydroxylation of coniferyl aldehyde, for modifying lignin b

iosynthesis, involves expressing the enzyme in a gymnosperm

Example 1; Page 61-64; 123pp; English.

The present sequence is that of sweetgum bifunctional O-met

hyltransferase (b1-OMP), as deduced from an isolated cDNA clone (see AAA86

683) enzyme is involved in the syringyl lignin biosynthetic path

way. The invention is to identify, sequence and clone specific g

enes involved in lignin production. The invention is to identify, sequence and clone specific g

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QY 61 TSDIASKLPPTKPPDAVMDRLRLRLASYSVLTCSLRTLPDCKIERLYGLAPVCKFLTEN 120
| | | | |
DB 61 TSDIASKLPPTKPPDAVMDRLRLRLASYSVLTCSLRTLPDCKIERLYGLAPVCKFLTEN 120
| | | | |
QY 121 DGVGSIALLSLMNQDKVLMESWYHLTEAVLEGIPFNKA YGWTAFEGHTDPRFNTVFN 180
| | | | |
DB 121 DGVGSIALLSLMNQDKVLMESWYHLTEAVLEGIPFNKA YGWTAFEGHTDPRFNTVFN 180
| | | | |
QY 181 GMSNSTITMKKILETYKGFEGLGSVDVGGTGAHLNMI IAKYPMIKGINFDLPVIEE 240
| | | | |
DB 181 GMSNSTITMKKILETYKGFEGLGSVDVGGTGAHLNMI IAKYPMIKGINFDLPVIEE 240
| | | | |
QY 241 APSYGEHVGGDMFVSPKGDALFMKWI CHDMSDEHCKFLPKCYEALPTNGKVILAE 300
| | | | |
DB 241 APSYGEHVGGDMFVSPKGDALFMKWI CHDMSDEHCKFLPKCYEALPTNGKVILAE 300
| | | | |
QY 301 ILPVPDASLPTKAVVHIDIVIMLAHNPCKERTKEFEALAKGAGFEGFRVVASCAVNTW 360
| | | | |
DB 301 ILPVPDASLPTKAVVHIDIVIMLAHNPCKERTKEFEALAKGAGFEGFRVVASCAVNTW 360
| | | | |
QY 361 IIEFLKKI 368
| | | | |
DB 361 IIEFLKKI 368
| | | | |

RESULT 3
AAE05829
ID AAE05829 standard; protein; 368 AA.
AC AAE05829;

DT 24-SEP-2001 (first entry)
XX L. scyractiflua angiosperm bifunctional-O-methyl transferase (bi-OMT).
XX

KW Sweetgum; angiosperm, bifunctional-O-methyl transferase; bi-OMT;
KW syringyl lignin; gymnosperm; pulp; papermaking; guaiacyl lignin;
XX delignification.
XX

OS Liquidambar scyractiflua.
XX

PN US6252135-B1.
XX

PD 26-JUN-2001.
XX

PF 16-DEC-1997; 97US-00991677.
XX

PR 16-DEC-1996; 96US-0033381P.
XX

PA (INTO) INT PAPER CO.
XX

PI Chiang VL, Carraway DT, Smeltzer RH;
XX

WPI: 2001-456503/49.
XX

DR N-PSDB; AAD11127.
XX

PT New P450-2 DNA encoding an enzyme involved in the biosynthesis of
PT syringyl lignin monomer units, for inducing the production of syringyl
PT lignin in gymnosperms and improving delignification for the production of
PT pulp.
XX

XX Example 1; Fig 2D-2E; 59pp; English.
XX

CC The invention relates to angiosperm sweetgum proteins bifunctional-O-
CC methyl transferase (bi-OMT). 4-coumarate CoA ligase (4CL), ferulic acid 5
CC -hydroxylase (P450-1 and P450-2) and their corresponding DNA molecules.
CC Angiosperm sweetgum proteins are useful for inducing the production of
CC syringyl lignin in gymnosperms for improved delignification in the
CC production of pulp for papermaking and other applications. The invention
CC also provides a method for modifying genes involved in lignin
CC biosynthesis in loblolly pine gymnosperms which involves cloning the
CC sweetgum DNA and fusing it to a constitutive promoter to form an

CC expression cassette. The expression cassette is then insert
CC gymnosperm genome, so that the production of syringyl lignin
CC while the production of guaiacyl lignin (less preferred for
CC suppressed. The present sequence is Liquidambar scyractiflua
CC bifunctional-O-methyl transferase (bi-OMT) protein
XX
SQ Sequence 368 AA;

Query Match 100.0%; Score 1915; DB 4; Length 36
Best Local Similarity 100.0%; Pred. No. 4.8e-196;
Matches 368; Conservative 0; Mismatches 0; Indels s 0;

QY 1 MGSITETKMSPEEAAAEEBAFVPMOLTSASVLMVLTSAIEEDVLEIM IS 60
| | | | |
DB 1 MGSITETKMSPEEAAAEEBAFVPMOLTSASVLMVLTSAIEEDVLEIM IS 60
| | | | |
QY 61 TSDIASKLPPTKPPDAVMDRLRLRLASYSVLTCSLRTLPDCKIERLYGL RN 120
| | | | |
DB 61 TSDIASKLPPTKPPDAVMDRLRLRLASYSVLTCSLRTLPDCKIERLYGL RN 120
| | | | |
QY 121 DGVGSIALLSLMNQDKVLMESWYHLTEAVLEGIPFNKA YGWTAFEGHT NN 180
| | | | |
DB 121 DGVGSIALLSLMNQDKVLMESWYHLTEAVLEGIPFNKA YGWTAFEGHT NN 180
| | | | |
QY 181 GMSNSTITMKKILETYKGFEGLGSVDVGGTGAHLNMI IAKYPMIKGI EE 240
| | | | |
DB 181 GMSNSTITMKKILETYKGFEGLGSVDVGGTGAHLNMI IAKYPMIKGI EE 240
| | | | |
QY 241 APSYGEHVGGDMFVSPKGDALFMKWI CHDMSDEHCKFLPKCYEALP EC 300
| | | | |
DB 241 APSYGEHVGGDMFVSPKGDALFMKWI CHDMSDEHCKFLPKCYEALP EC 300
| | | | |
QY 301 ILPVPDASLPTKAVVHIDIVIMLAHNPCKERTKEFEALAKGAGFEGFR TW 360
| | | | |
DB 301 ILPVPDASLPTKAVVHIDIVIMLAHNPCKERTKEFEALAKGAGFEGFR TW 360
| | | | |
QY 361 IIEFLKKI 368
| | | | |
DB 361 IIEFLKKI 368
| | | | |

RESULT 4
ADZ14866
ID ADZ14866 standard; protein; 368 AA.
AC ADZ14866;
XX
XX 16-JUN-2005 (first entry)
XX
XX DT Syringyl lignin production-related protein, SEQ ID NO: 6.
XX
XX DE Syringyl lignin production-related protein, SEQ ID NO: 6.
XX
XX KW Paper; lignin; genetic engineering.
XX
XX OS Unidentified.
XX
XX PN US2005076403-A1.
XX
XX PD 07-APR-2005.
XX
XX PF 09-OCT-2003; 2003US-00681878.
XX
XX PR 16-DEC-1996; 96US-0033381P.
XX
XX PR 16-DEC-1997; 97US-00991677.
XX
XX PR 28-FEB-2001; 2001US-00796256.
XX
XX PA (CHIA/) CHIANG V L.
XX
XX PA (CARR/) CARRAWAY D T.
XX
XX PA (SMEL/) SMELTZER R H.
XX
XX PI Chiang VL, Carraway DT, Smeltzer RH;
XX
XX DR WPI: 2005-272442/28.
XX
XX DR N-PSDB; ADZ14865.

XX Modifying a gymnosperm genome, useful for enhanced pulpability for
PT papermaking, comprises inserting into the gymnosperm an expression
PT cassette having genes which code for enzymes that produce syringyl lignin
PT monomer units.

PS Claim 27; SEQ ID NO 6; 60pp; English.

CC The present invention relates to a method for modifying the genome of a
CC gymnosperm. The method involves inserting into the gymnosperm an
CC expression cassette, formed by fusing cloned angiosperm DNA sequences
CC which code for genes necessary for production of angiosperm syringyl
CC lignin monomer units to a promoter region associated with a gene. The
CC invention is useful for enhanced pulpability for papermaking. The present
CC sequence is the syringyl lignin production-related protein. Note: The
CC SeqID numbers given in the sequence listing do not correspond to the
CC SeqID numbers given in the claims and figure descriptions of the
CC specification.

XX Sequence 368 AA;

Query Match 100.0%; Score 1915; DB 9; Length 368;
Best Local Similarity 100.0%; Pred. No. 4.8e-196;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSTETKMSPEEAAAEAEAFVFMQLTASVLPVLSAIELDVLEIMAKAGGAAHS 60
DB 1 MGSTETKMSPEEAAAEAEAFVFMQLTASVLPVLSAIELDVLEIMAKAGGAAHS 60
QY 61 TSDIASKLPPTKNPDAAVMDRLMLRLASYSVLTCSLRTPDGIKIRLYGLAVCKFLTRN 120
DB 61 TSDIASKLPPTKNPDAAVMDRLMLRLASYSVLTCSLRTPDGIKIRLYGLAVCKFLTRN 120
QY 121 DDGVSIAALSLMNODKVLMSWYHLTEAVLEGIPFNKAYGNTAFRYHGTDRFNTVFN 180
DB 121 DDGVSIAALSLMNODKVLMSWYHLTEAVLEGIPFNKAYGNTAFRYHGTDRFNTVFN 180
QY 181 GMSNSTITMKKILETYGFEGLGSVVDGCGTAHLNMIIAKYPIMIKINFDLPHVIEE 240
DB 181 GMSNSTITMKKILETYGFEGLGSVVDGCGTAHLNMIIAKYPIMIKINFDLPHVIEE 240
QY 241 APSYGVHEVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCYEALPTNGKYTLAEC 300
DB 241 APSYGVHEVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCYEALPTNGKYTLAEC 300
QY 301 ILPVAPDASLPTKAVVHIDVIMLANHNGKERTKEFEALAKAGFEGRRVVASCAVNTW 360
DB 301 ILPVAPDASLPTKAVVHIDVIMLANHNGKERTKEFEALAKAGFEGRRVVASCAVNTW 360
QY 361 IIEFLKKI 368
DB 361 IIEFLKKI 368

RESULT 5
AA01133
ID AA01133 standard; protein; 365 AA.

XX 25-MAY-1999 (first entry)
XX Aspen bispecific O-methyltransferase (OMT).
XX OMT; woody plant; enzyme; O-methyltransferase; wood color; furniture;
XX paper industry; lignin; wood pulping; aspen bispecific OMT.
XX Populus tremuloides.
XX US5886243-A.
XX 23-MAR-1999.

PF 18-SEP-1996; 96US-00715325.
XX 30-NOV-1995; 95US-0007727P.
XX (UNNT) UNIV MICHIGAN TECHNOLOGICAL.
XX Podila GK, Chiang VJC, Teal CJ;

DR MPI: 1999-228628/19.
DR N-PsDB; AAX26295.

PT Altering the wood color of a woody plant - by incorporating
PT methyltransferase gene into its genome, useful in the furni
PT industries.

PS Disclosure; Col 7-10; 9pp; English.

CC The invention relates to altering the wood color of a woody
CC incorporating a nucleotide sequence encoding the endogenous
CC enzyme O-methyltransferase (OMT) into its genome. Plants co
CC with altered wood color, are useful in the furniture and pai
CC and the modification of lignin caused by OMT (a reduction in
CC units) improves the efficiency of wood pulping. The present
CC represents an aspen bispecific OMT

XX Sequence 365 AA;

Query Match 83.3%; Score 1595.5; DB 2; Length 36
Best Local Similarity 80.9%; Pred. No. 9.3e-162;
Matches 297; Conservative 37; Mismatches 30; Indels

QY 1 MGSTETKMSPEEAAAEAEAFVFMQLTASVLPVLSAIELDVLEIM 60
DB 1 MGSTETKMSPEEAAAEAEAFVFMQLTASVLPVLSAIELDVLEIM 60
QY 61 TSDIASKLPPTKNPDAAVMDRLMLRLASYSVLTCSLRTPDGIKIRLYGL 120
DB 61 TSDIASKLPPTKNPDAAVMDRLMLRLASYSVLTCSLRTPDGIKIRLYGL 120
QY 121 DDGVSIAALSLMNODKVLMSWYHLTEAVLEGIPFNKAYGNTAFRYHGT 180
DB 121 DDGVSIAALSLMNODKVLMSWYHLTEAVLEGIPFNKAYGNTAFRYHGT 180
QY 181 GMSNSTITMKKILETYGFEGLGSVVDGCGTAHLNMIIAKYPIMIKIN 240
DB 181 GMSNSTITMKKILETYGFEGLGSVVDGCGTAHLNMIIAKYPIMIKIN 240
QY 241 APSYGVHEVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCYEALP 300
DB 241 APSYGVHEVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCYEALP 300
QY 301 ILPVAPDASLPTKAVVHIDVIMLANHNGKERTKEFEALAKAGFEGRR 360
DB 301 ILPVAPDASLPTKAVVHIDVIMLANHNGKERTKEFEALAKAGFEGRR 360
QY 361 IIEFLKK 367
DB 361 IIEFLKK 364

RESULT 6
AAU80015
ID AAU80015 standard; protein; 365 AA.

XX 15-JUL-2002 (first entry)
XX 5-hydroxyconiferaldehyde O-methyltransferase (AldOMT).
XX Plant; aspen; phenylpropanoid pathway; agronomic; lignin; p
XX 4-coumarate-CoA ligase; 4Cl; conifer; aldehyde 5-hydroxylat
XX S-adenosyl-L-methionine-dependent; SAM; AldOMT; transgenic;

paper

lign
OMT,
tries
/1

TS 60
JS 58

UN 120

CN 118

UN 180

UK 178

SE 240

SD 238

3C 300

3C 298

FW 360

TH 357

3H;

5-hydroxyconiferaldehyde O-methyltransferase; cellulose; pulp; coniferyl alcohol dehydrogenase; CAD; sinapyl alcohol dehydrogenase; SAD; syringyl; guaiacyl; agriculture.

Populus tremuloides.

MO20020717-A2.

14-MAR-2002.

05-SEP-2001; 2001WO-US027445.

05-SEP-2000; 2000US-0230086P.

(UNMT) UNIV MICHIGAN TECHNOLOGICAL.

Chiang VLC, Li L;

WPI; 2002-351773/38.

N-PSDB; ABK48067.

Genetically transforming plant with multiple genes from phenylpropanoid pathways, comprises incorporating number of genes into the genome of the plant, to produce plants displaying altered agronomic traits.

Example 2; Fig 4B; 95pp; English.

The invention relates to a method of genetically transforming a plant simultaneously with multiple genes from the phenylpropanoid pathways, comprising incorporating into the genome of the plant, a number of genes, their substantially similar fragments or their combinations, to produce plants displaying altered agronomic traits. The genes are selected from 4 -coumarate-CoA ligase (4CL), coniferyl aldehyde 5-hydroxylase (CA15H), S -adenosyl-L-methionine (SAM)-dependent 5-hydroxyconiferaldehyde O -methyltransferase (AldOMT), coniferyl alcohol dehydrogenase (CAD) and sinapyl alcohol dehydrogenase (SAD). The method is useful for the transformation of plant tissue for the alteration of lignin monomer composition, increased syringyl/guaiacyl (S/G) lignin ratio and increased cellulose content and transgenic plants resulting from such transformations. This is an improved method to simultaneously control the lignin quantity, lignin compositions, and cellulose contents in plants, and is applicable to all plant species that are susceptible to the transfer of genetic information by Agrobacterium or other gene delivery system. The method is of particular value to paper and pulp industries because lignin containing higher syringyl monomer content is more susceptible to chemical delignification. Woody plants transformed with DNA constructs offer a significant advantage in the delignification process over conventional paper feedstocks. Similarly, modification of the lignin composition in grasses by insertion and expression of heterologous SAD gene offers a unique method for increasing the digestibility of grasses and is of significant potential economic benefit to the farm and agricultural industries. The present sequence represents the amino acid sequence of 5-hydroxyconiferaldehyde O-methyltransferase (AldOMT) used in the method of the invention

Sequence 365 AA;

Query Match 83.3%; Score 1595.5; DB 5; Length 365; Best Local Similarity 80.9%; Pred. No. 9.3e-162; Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;

1 MGSSTETMSSEAAAEERAFVPMQUTSASVLPVWLKSAIELDVLEIMAKAGGAHIS 60
1 MGSSTETMTPTO--VSDDEBAHLFPMQULASASVLPVWLKSAIELDVLEIMAKAGGAFIS 58

1 TSDTASLPTNPPAAVWLDRMLRLASVLTCSLRTLPQGIERYGLAPVCKEFLRN 120
1 TSDTASLPTNPPAAVWLDRMLRLASVLTCSLRTLPQGIERYGLAPVCKEFLRN 118

121 DDGVSIALSLMNDKVLMSWYHLTEAVLEGGIPFNKAYGWTAFYHGTDPREFTVFN 180
121 DDGVSIALSLMNDKVLMSWYHLTEAVLEGGIPFNKAYGWTAFYHGTDPREFTVFN 178

181 GMSNSTITMKILITTYGFBGLSVVDVGGTGALHNLIAKYPMTIKI
179 GMSDSTITMKILITTYGFBGLSVVDVGGTGAVVMTIVAKYPSIKI

241 APSYGEVHGDMVSPKGAIFMKWICHMSPDHCKFLKCKYBALP
239 APSYGEVHGDMVSPKGAIFMKWICHMSPDHCKFLKCKYBALP

301 ILVAPDASLPTKAVHIDVIMLANPGKERTKEFEALAKAGAFEGFR
299 ILVAPDASLPTKAVHIDVIMLANPGKERTKEFEALAKAGAFEGFR

361 IIEFLKK 367
358 VIEFRKK 364

RESULT 7
ADD93900 standard; protein; 365 AA.
ADD93900;
29-JAN-2004 (first entry)

Quaking aspen AldOMT protein.

Quaking aspen; Plant; enzyme; 4-coumarate-CoA ligase; 4CL; coniferyl aldehyde 5-hydroxylase; CA15H; SAM-dependent 5-hydroxyconiferaldehyde O-methyltransferase; S-adenosyl-L-methionine; AldOMT; coniferyl alcohol dehydrog sinapyl alcohol dehydrogenase; SAD; transgenic; agronomic p lignin; cellulose; syringyl/guaiacyl lignin ratio; growth; w stress resistance; sterility; grain yield; nutritional valu paper delignification; pulp manufacture; grass digestibilit

Populus tremuloides.

US2002138870-A1.

26-SEP-2002.

06-MAR-2002; 2002US-00091009.

05-SEP-2000; 2000US-0230086P.
05-SEP-2001; 2001US-00947027.

(UNMT) UNIV MICHIGAN TECHNOLOGICAL.

Chiang VLC, Li L;

WPI; 2003-843045/78.
N-PSDB; ADD93899.

Genetic transformation of plants, useful for altering ligni cellulose contents, by introducing genes from the phenylpro pathways, also new transgenic plants.

Disclosure: SEQ ID NO 6; 55pp; English.

The invention relates to the genetic transformation of a pl simultaneously with several genes from the phenylpropanoid incorporating into the genome the genes for 4-coumarate-CoA coniferyl aldehyde 5-hydroxylase (CA15H), S-adenosyl-L-Met hydroxyconiferaldehyde O-methyltransferase (AldOMT), confie dehydrogenase (CAD) and sinapyl alcohol dehydrogenase (SAD) fragments or combination to produce plants with altered agr Also included are preparing plant cells that contain, in th several DNA constructs containing one or more of the specif preparing transgenic plants with altered lignin or cellulose of the regenerated plant), transgenic plants produced by me their progeny, plants that include in the genome a construct

EE 240
ED 238
EC 300
EC 298
TW 360
TH 357

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(4CL),
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at least one of the specified gene (linked to a promoter and a terminator), a set of DNA constructs (each containing a promoter, terminator and at least one of the specified genes or their fragments) and the set of above or a single construct containing the 4CL gene, where incorporated into a plant genome. The method is used to transform plants, particularly trees but also forage crops and monocotyledons, to alter their agronomic properties, especially lignin and cellulose contents, syringyl/quinic acid (S/G) lignin ratio, growth, wood quality, stress resistance, sterility, grain yield and nutritional value, particularly to increase S/G ratio (this simplifies delignification in paper and pulp manufacture) and to increase digestibility of grasses. The present sequence represents quaking aspen Aldomt.

Sequence 365 AA;

Query Match 83.3%; Score 1595.5; DB 7; Length 365;
Best Local Similarity 80.9%; Pred. No. 9.3e-162;
Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;

```

1 MGSSTETKSPSEAAAEBAFVPMOLTSASVLPVMTKSAIELEVLIMAKAGRGATIS 60
1 MGSSTETKMTPTQ--VSDEBAHLPFMOLASVLPMLKTAIELEVLIMAKAGRGATIS 58
61 TSDIASKLPTKNPDPAVMDRLMLLASVYLTSGLRTLPGDKIBRLYGLAPVCKFLTRN 120
59 TSEIASHLPKNPDPAVMDRLMLLASVYLTSGLRTLPGDKIBRLYGLAPVCKFLTRN 118
121 DDGVSIALLSMNQDKVLMESWYHLTEAVLEGGIFPNKAYGMTAFEHYGTDPREYTVNN 180
119 EDGVSIVSLCLMNQDKVLMESWYHLKDAILDGGIFPNKAYGMTAFEHYGTDPREYTVNN 178
181 GMSNSTITMKKILETYKGFEGLSVVDVGGGTGAHLNMIIAKYPMIGINDLPHVIEE 240
179 GMSDSTITMKKILETYKGFEGLSVVDVGGGTGAHVNTIVSKYSIKGINPDLPHVIED 238
241 APSYGEVHVGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEALPTNGVYILAEC 300
239 APSYGEVHVGDMFVSVPKADAVFMKWI CHDMSDAHCKFLKNCYALDPENGVYILVEC 298
301 ILPVPADSLPTKAVVHIDVIMLANPGGKERTKTEFEFALAKGAGFEGRRVVASCAVNTW 360
299 ILPVPADTSLATKGVVHIDVIMLANPGGKERTKTEFEFALAKGAGFEGRRVVASCAVNTW 357
361 IIEFLKK 367
358 VIEFLKK 364

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RESULT 8
AA030114
ID AA030114 standard; protein; 365 AA.

```

AC AA030114;
AC XX
AC XX
DT 03-SEP-2003 (first entry)
DT XX
DE Strawberry O-methyltransferase (STOMT).
DE XX
KW Strawberry; O-methyltransferase; 2,5-dimethyl-4-hydroxy-3(2H)-furanone;
KW STOMT; DMHF; dihydrotheitol; 2,5-dimethyl-4-methoxy-3(2H)-furanone; DTF;
KW DMHF; enzyme; plant.
KW XX
XX Fragaria x ananassa.
XX XX
XX WO2003046163-A2.
XX XX
XX 05-JUN-2003.
XX XX
XX 26-NOV-2002; 2002MO-EP013320.
XX XX
XX 26-NOV-2001; 2001US-0332534P.
XX XX
XX (UYBA-) UNIV BAYERISCHE JULIUS MAXIMILIANS WUERZ.
XX PA

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xx Schwab W, Kaldenhoff R, Wein M;
xx MPI; 2003-532772/50.
xx N-PSDB; AAL60735.
xx Novel isolated strawberry O-methyltransferase polypeptide u
xx methylating ortho-dihydroxy substituted ring system such as
xx caffeic acid, protocathechin aldehyde or pyrogallol.
xx
xx Claim 1; Page 76-77; 78pp; English.

xx The invention relates to novel strawberry O-methyltransfera
xx polypeptides capable of methylating an ortho-dihydroxy subst
xx system and nucleic acid molecules encoding such polypeptide
xx invention is useful for methylation of an ortho-dihydroxy su
xx ring system and/or its mimetics (such as 2,5-dimethyl-4-hy
xx furanone (DMHF) or dihydrotheitol (DTT)). The invention is
xx for the synthesis of naturally occurring substances preferal
xx compounds such as 2-methoxyphenol, vanillin, ferulic acid,
xx DMHF, for enhancing the function of naturally-occurring STY
xx or tissue cultured cells, or to enhance the production of f
xx enhancing substances such as vanillin or 2,5-dimethyl-4-met
xx furanone (DMHF). The present sequence is Fragaria x ananassa
xx O-methyltransferase

Sequence 365 AA;

Query Match 83.0%; Score 1589.5; DB 6; Length 36
Best Local Similarity 81.0%; Pred. No. 4.1e-161;
Matches 298; Conservative 39; Mismatches 28; Indels

```

1 MGSSTETKSPSEAAAEBAFVPMOLTSASVLPVMTKSAIELEVLIM 60
1 MGSSTETKMTPTQ--VSDEBAHLPFMOLASVLPMLKTAIELEVLIM 58
61 TSDIASKLPTKNPDPAVMDRLMLLASVYLTSGLRTLPGDKIBRLYGL 120
59 PSDIASQLPTKNPDPAVMDRLMLLASVYLTSGLRTLPGDKIBRLYGL 118
121 DDGVSIALLSMNQDKVLMESWYHLTEAVLEGGIFPNKAYGMTAFEHYGT 180
119 EDGVSIALCLMNQDKVLMESWYHLKDAILDGGIFPNKAYGMTAFEHYGT 178
181 GMSNSTITMKKILETYKGFEGLSVVDVGGGTGAHLNMIIAKYPMIGII 240
179 GMSDSTITMKKILETYKGFEGLSVVDVGGGTGAHVNTIVSKYSIKGIN 238
241 APSYGEVHVGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEALP 300
239 APQYGVHVGDMFVSVPKGNALFMKWI CHDMSDEHCLKFLKNCYALPI 298
301 ILPVPADSLPTKAVVHIDVIMLANPGGKERTKTEFEFALAKGAGFEGRR 360
299 ILPVPADTSLATKGVVHIDVIMLANPGGKERTKTEFEFALAKGAGFEGRR 357
361 IIEFLKKI 368
358 VIEFLKKI 365

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RESULT 9
AAW84132
ID AAW84132 standard; protein; 365 AA.

```

AC AAW84132;
AC XX
AC XX
DT 11-FEB-1999 (first entry)
DT XX
DE Exemplary caffeic acid methyl transferase COMT sequence.
DE XX
XX (iso) eugenol methyl transferase; IEMT; lignin reduction;
XX phenylpropanoid biosynthetic pathway; methyl-iso Eugenol;
KW

```

KM caffeic acid methyl transferase; COMT.
XX
OS unidentified.
XX
PN MO980570-A2.
XX
PD 12-NOV-1998.
XX
PF 08-MAY-1998; 98WO-US009522.
XX
PR 08-MAY-1997; 97US-0046857P.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Picheraky E, Wang J;
XX
XX WPI, 1998-610385/51.
XX
PT New isolated (iso)eugenol methyl transferase nucleic acids - used for
PT increasing methyl-isoegenol, decreasing the (iso)eugenol content of, or
PT decreasing lignin biosynthesis in, plants.
XX
XX Disclosure; Page 123-124; 151pp; English.
XX
XX The present sequence represents an exemplary caffeic acid methyl
CC transferase COMT sequence. The specification describes a Clarksia breweri
CC (iso) eugenol methyl transferase (IEMT) enzyme. IEMT catalyzes the
CC methylation of the para-4'-hydroxyl of both eugenol and isoegenol to
CC methyl-eugenol and methyl-isoegenol, and participates in the
CC phenylpropanoid biosynthetic pathway. The IEMT nucleic acid can be used
CC for increasing the synthesis of methyl-isoegenol in plant cells or for
CC decreasing the (iso)eugenol content of plant cells. IEMT expression or
CC overexpression may facilitate the increased production of other desirable
CC products such as vanillin. The nucleic acids can also be used for
CC producing plants with a reduced amount of lignin which would be more
CC efficiently used as crop plants or fodder plants and which may have
CC increased yields when lignin has a negative effect on plant growth
XX
XX Sequence 365 AA;

Query Match 83.0%; Score 1588.5; DB 2; Length 365;
Best Local Similarity 80.7%; Pred. No. 5,2e-161;
Matches 296; Conservative 37; Mismatches 31; Indels 3; Gaps 2;
QY 1 MGSTSETMSPSEAAAEEBAFVPMQUTSASVLPVTKSAIEDVLEIMAKAGAHIS 60
DB 1 MGSTGETMTPTQ--VSDEBAHLFAMQLASASVLPMLIKTAIEDLLRIMAKAGGAF 58
QY 61 TSDIASKLPTKNPDAVNLDRMLRLASYSVLTGSLRTLPGCKIRLGLAPVCKEFLRN 120
DB 59 TSEIASHLPTKNPDAVNLDRILRLASYSILTCSLKLPDCKVRLGLAPVCKEFLRN 118
QY 121 DDGVSIALSLMNDKVLMSWYHLTEAVLEGGIPFNKAYGMTAFEGYGTDPREFTVFN 180
DB 119 EDGVSVSPLCLMNGDKVLMESWYILKDAILOGGIPFNKAYGMTAFEGYGTDPREFTVFN 178
QY 181 GMSNSTITMKKILLETYKGFEGLSVVDVGGGTGAHLNMIATAKPYMIKGINFDLEPHV 240
DB 179 GMSHSTITMKKILLETYKGFEGLSVVDVGGGTGAHVNTIVSKYPSIKGINFDLEPHV 238
QY 241 APSYGVHVGDMFVSPKGDALFMKVICHDMSDEHLKFLKCCYEALPTNKGKTIILAE 300
DB 239 APSYGVHVGDMFVSPKADAVPMKVICHDMSDEHLKFLKCCYEALPTNKGKTIILAE 298
QY 301 ILVAPDASLPTKAVHIDVIMLANPGKERTKEFEALAKGAGFEGFRVASCAYNTM 360
DB 299 ILVAPDASLPTKAVHIDVIMLANPGKERTKEFEALAKGAGFEGFRVASCAYNTM 357
QY 361 IIEFLKK 367
DB 358 VIEFRKK 364

RESULT 10
AAR34762
ID AAR34762 standard; protein; 364 AA.
XX
AC AAR34762;
XX
DT 25-MAR-2003 (revised)
DT 16-JUL-1993 (first entry)
XX
DE pPLC4 translation product.
XX
KM Plasmid, clone; pPLC4; transformation vector; CAD; enzyme;
KM caffeic acid O-methyl transferase; OMT; biosynthesis; diges
KM fodder; cattle; stalk strength; resistance; disease.
XX
OS Synthetic.
XX
PN MO9305160-A1.
XX
PD 18-MAR-1993.
XX
PF 09-SEP-1992; 92WO-GB001640.
XX
PR 10-SEP-1991; 91GB-00019279.
XX
PA (ICIL) IMPERIAL CHEM IND PLC.
XX
PI Van Doorselaere J, Fritig GJ, Inze DG, Jouanin L, Knig
PI Van Montagu M, Legrand M;
XX
DR WPI, 1993-100983/12.
DR N-PSDB; AA038448.
XX
PT DNA for modifying lignin content of plants - encodes o-meth
PT enzyme which can be enhanced or inhibited in plants, e.g. f
XX
PS Disclosure; Fig 1; 46pp; English.
XX
XX The sequence given represents the product of plasmid clone
CC can be used to produce a transformation vector for insertio
CC to regulate the production of the CAD enzyme. This sequence
CC caffeic acid O-methyl transferase (OMT) and can be used to
CC by modifying lignin biosynthesis. An anti-sense construct
CC sequence will down-regulate lignin synthesis. This is espec
CC for improving the digestibility of fodder crops for cattle.
CC production of lignin by a sense construct may improve plant
CC strength and resistance to disease. (Updated on 25-MAR-2003
CC field.)
XX
XX Sequence 364 AA;

Query Match 82.4%; Score 1578.5; DB 2; Length 3
Best Local Similarity 80.6%; Pred. No. 6,2e-160;
Matches 295; Conservative 36; Mismatches 32; Indels
QY 1 MGSTSETMSPSEAAAEEBAFVPMQUTSASVLPVTKSAIEDVLEIM 60
DB 1 MGSTGETMTPTQ--VSDEBAHLFAMQLASASVLPMLIKTAIEDLLRIM 58
QY 61 TSDIASKLPTKNPDAVNLDRMLRLASYSVLTGSLRTLPGCKIRLGL 120
DB 59 TSEIASHLPTKNPDAVNLDRILRLASYSILTCSLKLPDCKVRLGL 118
QY 121 DDGVSIALSLMNDKVLMSWYHLTEAVLEGGIPFNKAYGMTAFEGYGT 180
DB 119 EDGVSVSPLCLMNGDKVLMESWYILKDAILOGGIPFNKAYGMTAFEGYGT 178
QY 181 GMSNSTITMKKILLETYKGFEGLSVVDVGGGTGAHLNMIATAKPYMIKGI 240
DB 179 GMSHSTITMKKILLETYKGFEGLSVVDVGGGTGAHVNTIVSKYPSIKGI 238
QY 241 APSYGVHVGDMFVSPKGDALFMKVICHDMSDEHLKFLKCCYEALP 300

Db 239 APSYGVGEHVGDMFVSVPKADAFPMKMICHDWSDAHCLKFKNGCYDALPENGKVIIVEC 298
QY 301 ILPVPDASLPTKAVNHIDVIMLANPGKERTKEFEFLAKGAFEGPRVASCANYTW 360
Db 299 ILPVAPDSLSLATKGVHIDVIMLANPGKERTKEFEFLAKGAFQGEVWC-CAFNTH 357
QY 361 IIEFLKX 366
Db 358 VIEFLKX 363

RESULT 11

AAE16510
ID AAE16510 standard; protein; 365 AA.
XX AAE16510;

DT 09-APR-2002 (first entry)

DE Soybean caffeic acid 3-O-methyltransferase (COMT) #1.

KM Soybean; caffeic acid 3-O-methyltransferase; COMT; caffeic acid;
KM 5-hydroxyferulic acid O-methyl transferase; phenylpropanoid;
KM transgenic plant; 5-hydroxyferulic acid; injury-repair mechanism;
KM papermaking; host defect repair mechanism; lignin biosynthesis.

OS Glycine max.

XX US6329204-B1.

XX PD 11-DEC-2001.

XX PF 09-FEB-2000; 2000US-00500569.

XX PR 10-FEB-1999; 99US-0119587P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Cahoon RE, Rafalski JA, Shen JB;

XX DR WPI; 2002-121138/16.

XX DR N-PSDB; AAD27040.

PT New polynucleotide encoding caffeic acid 3-O-methyltransferase from rice,
PT useful for studying lignin biosynthesis and in positive selection
PT systems.

XX Example 3; Page 27-30; 34pp; English.

CC The invention relates to an isolated nucleic acid fragment encoding
CC caffeic acid 3-O-methyltransferase (COMT) (also known as caffeic acid/5-
CC hydroxyferulic acid O-methyl transferase) involved in phenylpropanoid
CC metabolism. COMT is involved in the biosynthesis of the mono- or
CC dimethoxylated lignin precursors. COMT DNA is used to produce transgenic
CC plants or microbes that have altered levels of methylation for both
CC caffeic and 5-hydroxyferulic acids, so can provide a method for positive
CC selection. Since caffeic acid 3-O-methyltransferase is involved in lignin
CC biosynthesis, the transgenic plants may have altered contents, or types,
CC of lignin, so may be better suited for papermaking, and COMT DNA can also
CC be used to study synthesis of lignin in plant cells, including its role
CC in host defect- and injury-repair mechanisms. The present sequence is
CC soybean COMT protein

XX Sequence 365 AA;

QY Query Match 81.8%; Score 1566.5; DB 5; Length 365;

CC Best Local Similarity 80.2%; Pred. No. 1.2e-158;

CC Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGSTSETGMSBEAABAEAFVFMOLTSASVLMVLTLSALEVLEIMAAAGCAHIS 60

Db 1 MGSTGETGTTPTTH--VSDSEANLFAWQLASASVLPMLTKSALDLTLTIAKAGGVHLS 58

QY 61 TSDIASKRLPTQNPAAVWLDLMDRLRLASYSVLTCISRTLPGKIERLYGL
Db 59 PTDISSQLPTQNPAPVWLDRLRLRLACTYNTLSBSRLTLPDGKVRGLGL
QY 121 DDGVSAIALSLMNDQKVLMSWYHLTEAVLEGGLPEFNKAYGWTAEYHGT
Db 119 EDGVSAIALNLMDQKVLMSWYHLKDAVLEGGLPEFNKAYGWTAEYHGT
QY 181 GMSNSTITMKKILLETYGFEGSLGSVVDVGSGTGAGHMLMIAKYMIMGII
Db 179 GMADSTITMKKILLETYGFESLSKLVVDVGSGTGAVIMMIVSKHPTINGII
QY 241 APSYGVGEHVGDMFVSVPKADAFPMKMICHDWSDERHCLKFKKCYEALP
Db 239 APSYGVGEHVGDMFVSVPKADAFPMKMICHDWSDERHCLKFKKCYEALP
QY 301 ILPVPDASLPTKAVNHIDVIMLANPGKERTKEFEFLAKGAFEGPR
Db 299 ILPVAPDSLSLATKGVHIDVIMLANPGKERTKEFEFLAKGSGQGFRI
QY 361 IIEFLKX 366
Db 358 IIEFLKX 365

RESULT 12

AD129674
ID AD129674 standard; protein; 365 AA.

XX AD129674;

XX DT 22-APR-2004 (first entry)

DE Soybean caffeic acid 3-O-methyltransferase homologue sequen
XX caffeic acid 3-O-methyltransferase; phenylpropanoid metabol
KM transgenic plant; enzyme; soybean.

XX Glycine max.

XX US6610521-B1.

XX PD 26-AUG-2003.

XX PF 05-OCT-2001; 2001US-00971823.

XX PR 10-FEB-1999; 99US-0119587P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Cahoon RE;

XX DR WPI; 2003-895338/82.

XX DR N-PSDB; AD129673.

PT New polynucleotide having a sequence encoding a polypeptide
PT caffeic acid 3-O-methyltransferase activity, useful for prok
PT levels of the protein involved in phenylpropanoid metabolis
PT transformed host cell.

XX Claim 4; SEQ ID NO 4; 35pp; English.

CC This invention relates to a novel isolated polynucleotide w
CC a nucleotide sequence or its complement encoding a polypept
CC activity of caffeic acid 3-O-methyltransferase. The amino ac
CC of the polypeptide has at least 92% identity with the fully
CC amino acid sequence based on the clustal alignment method.
CC polynucleotide is useful for producing altered levels of th
CC involved in phenylpropanoid metabolism in a transformed hos
XX Sequence 365 AA;

Query Match 81.8%; Score 1566.5; DB 7; Length 365;
Best Local Similarity 80.2%; Pred. No. 1.2e-158;
Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;

DB 1 MGSTSETKMSPEBAABEAFVPMQLTASVLPVLSAIEIDVLEITMAKAGQAHIS 60
1 MGSTGETQITPTH--VSDBEANTLPMQLASASVLEMLKSALELDLEITAKGQVHIS 58
61 TSDIASKLPTKNDPAVMDRLMLRLASYSVLTCSLRTLPGDKIERLYGLAPVCKELTN 120
59 PTDISSQLPTQNPDPAPVMDRLRLRLACVNIISFSLRTLPGDKVERLYGLAPVAKYLVKN 118
121 DDGVSIALSLMNOKVLMESWYHLTEAVLBEGIFPNKAYGWTAREYHTDPRPTVFN 180
119 EDGVSIALSLMNOKVLMESWYHLTKDAVLREGIFPNKAYGTAREYHTDPRFNK 178
181 GMSNSTITMKKILETYKGFEGISVVDVGGTGANLNMIIAKYPMIKINPDLPHVIE 240
179 GMAHSTITMKKILETYGFESLKSVDVGGTGAVIMIVSKHTIKINPDLPHVIED 238
241 APSYGVHEHVGDMFVSVPKGDALFMKWI CHDMSDEHCLKFKCYEALPTNGKVI LAEC 300
239 APSYGVHEHVGDMFVSVPKADALFMKWI CHDMSDEHCLKFKCYEALPDNGKVI VAEC 298
301 ILPVPDASLPTKNAVHIDVIMLANPBGKERTKEKFEFALAKGAGPEGRRVVASCAVNTW 360
299 ILPVPDSSLATKGVVHIDVIMLANPBGKERTKEKFEFALAKGSGFQGRVVC-CAFTYN 357
361 IIEFLKKI 368
358 IMEFLKKI 365

RESULT 13
ADJ96484
ID ADJ96484 standard; protein; 365 AA.

AC ADJ96484;
DT 06-MAY-2004 (first entry)
XX Soybean caffeic acid 3-O-methyltransferase protein #1.
XX Caffeic acid 3-O-methyltransferase; COMT;
KW caffeic acid/5-hydroxyferulic acid O-methyltransferase;
KW caffeoyl CoA 3-O-methyltransferase; COMT; lignin production;
KW cell wall architecture; host defense; injury repair mechanism;
KW transgenic plant; plant; soybean; enzyme.
XX Glycine max.
OS US2004014116-A1.
XX
XX 22-JAN-2004.
XX
XX 17-JUN-2003; 2003US-00464610.
XX
XX 10-FEB-1999; 99US-0119587P.
XX 09-FEB-2000; 2000US-00500569.
XX 05-OCT-2001; 2001US-00971823.
XX
XX (CAHO/) CAHOON R E.
XX (RAFA/) RAFALSKI J A.
XX (SHEN/) SHEN J B.
XX
XX Cahoon RE, Rafalski JA, Shen JB;
XX
XX WPI; 2004-121565/12.
XX N-PSDB; ADJ96483.
XX
XX New polynucleotide encoding a caffeic acid 3-O-methyltransferase
XX polypeptide, useful in controlling lignin production in plant cells to
XX control cell wall architecture and host defense and injury repair

PT mechanisms in plant cells.
XX
XX PS Claim 10; SEQ ID NO 4; 38pp; English.
XX
XX The present invention relates to isolated polypeptide caffe
CC methyltransferase (COMT) and the encoding polynucleotide. T
CC otherwise termed as caffeic acid/5-hydroxyferulic acid O-
CC methyltransferase and caffeoyl CoA 3-O-methyltransferase (C
CC invention is useful in controlling lignin production in pla
CC control cell wall architecture and host defense and injury
CC mechanisms in plant cells. The invention is also useful in
CC transgenic plants with altered level of methylation of caff
CC hydroxyferulic acid. The present sequence is caffeic acid
CC methyltransferase (COMT) protein.
XX
XX SQ Sequence 365 AA;

Query Match 81.8%; Score 1566.5; DB 8; Length 3
Best Local Similarity 80.2%; Pred. No. 1.2e-158;
Matches 295; Conservative 41; Mismatches 29; Indels 3

QY 1 MGSTSETKMSPEBAABEAFVPMQLTASVLPVLSAIEIDVLEIM 1S 60
1 MGSTGETQITPTH--VSDBEANTLPMQLASASVLEMLKSALELDLEIT 1S 58
61 TSDIASKLPTKNDPAVMDRLMLRLASYSVLTCSLRTLPGDKIERLYGL RN 120
59 PTDISSQLPTQNPDPAPVMDRLRLRLACVNIISFSLRTLPGDKVERLYGL KN 118
121 DDGVSIALSLMNOKVLMESWYHLTEAVLBEGIFPNKAYGWTAREYGT NN 180
119 EDGVSIALSLMNOKVLMESWYHLTKDAVLREGIFPNKAYGTAREYHT NK 178
181 GMSNSTITMKKILETYKGFEGISVVDVGGTGANLNMIIAKYPMIKI EE 240
179 GMAHSTITMKKILETYGFESLKSVDVGGTGAVIMIVSKHTIKI ED 238
241 APSYGVHEHVGDMFVSVPKGDALFMKWI CHDMSDEHCLKFKCYEALP EC 300
239 APSYGVHEHVGDMFVSVPKADALFMKWI CHDMSDEHCLKFKCYEALP EC 298
301 ILPVPDASLPTKNAVHIDVIMLANPBGKERTKEKFEFALAKGAGPEGRR TW 360
299 ILPVPDSSLATKGVVHIDVIMLANPBGKERTKEKFEFALAKGSGFQGR TW 357
361 IIEFLKKI 368
358 IMEFLKKI 365

RESULT 14
AAR63203
ID AAR63203 standard; protein; 365 AA.
XX
XX AAR63203;
XX
XX 25-MAR-2003 (revised)
XX 10-MAY-1995 (first entry)
XX
XX Alfaifa COMT.
XX Alfaifa; tobacco; Nicotiana tabacum; crop improvement; COMT
KW caffeic-acid-3-O-methyltransferase; lignin; pCOMT; antiseen
XX Medicago sativa.
XX
XX WO9423044-A1.
XX
XX 13-OCT-1994.
XX
XX 31-MAR-1994; 94MO-US003356.
XX 02-APR-1993; 93US-00045263.

Mon Dec 12 10:52:55 2005

us-10-681-878a-6.rag

ge 11

Search completed: December 12, 2005, 08:33:30
Job time : 194 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 08:27:04 ; Search time 39 Seconds
(without alignments)
907.892 Million cell updates/sec

Title: US-10-681-878A-6

Perfect score: 1915

Sequence: 1 MGSTSETKMSPEAAASEE.....FRVASCANWTWIFLKKI 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1595.5	83.3	365	2	S18568
2	1544.5	80.7	365	2	T09673
3	1535	80.2	366	2	S40146
4	1527.5	79.8	359	2	T13259
5	1510	78.9	364	2	T09780
6	1499.5	78.3	364	2	S36403
7	1484.5	77.5	364	2	S16404
8	1403.5	73.3	350	2	T12260
9	1185	61.9	364	2	S28612
10	1062.5	55.5	365	2	J02344
11	1047	54.7	365	2	S22696
12	836	43.7	372	2	T09617
13	832	43.4	363	2	E96559
14	831.5	43.4	381	2	G96804
15	830.5	43.4	381	2	F96804
16	811.5	42.0	352	2	H86454
17	803.5	42.0	373	2	E86344
18	794.5	41.5	373	2	B86344
19	789.5	41.3	373	2	D86344
20	789.5	41.2	373	2	C86344
21	780.5	40.8	381	2	H96966
22	736.5	38.5	367	2	E96795
23	711	37.1	382	2	T09600
24	686.5	35.8	376	2	T06189
25	596	31.1	359	2	T46160
26	510	26.6	382	2	E96653
27	456	23.8	382	2	T04963
28	402	21.0	352	2	T09707
29	396.5	20.7	325	2	T04962

30	393	20.5	352	2	T09254	isoetl	O-met
31	378	19.7	364	2	UQ2268	O-met	feras
32	376	19.6	360	2	T06786	6a-hy	ckial
33	369	19.3	390	2	S52015	chylt	chylt
34	354.5	18.5	343	2	T09299	catec	feras
35	352	18.8	376	2	J01393	O-dem	omcyl
36	289	15.1	341	2	JC5855	polylk	nthas
37	272.5	14.2	366	2	T01354	heizl	ener
38	255.5	13.3	346	2	S21265	acetyl	in O-
39	252.5	13.2	345	2	A42106	acetyl	in O-
40	252.5	13.2	494	2	S27696	lcml	Str
41	202.5	10.6	373	2	I37463	acetyl	in O-
42	186.5	9.7	356	2	A47128	carri	4-O-m
43	179.5	9.4	376	2	S49626	crte	- Rho
44	179	9.3	334	2	F83120	proba	chylt
45	178	9.3	339	2	F70932	hypot	prote
46	174	9.1	393	2	S04408	poren	poren
47	171	8.9	379	2	T50751	hydro	poren
48	159	8.3	292	2	JC4099	hypot	32.1k
49	158	8.3	390	2	T50880	hypot	poren
50	139	7.3	339	2	C42276	hydro	feras
51	116.5	6.1	270	2	E69303	metly	rase
52	111	5.8	1353	2	T00249	metly	rase
53	105	5.5	352	2	E86015	ichl	chylt
54	101.5	5.3	363	2	A10184	proba	r ABC
55	100.5	5.2	308	2	S72886	hypot	prote
56	100.5	5.2	487	1	A64472	catba	sphat
57	100	5.2	372	2	F64310	hypot	prote
58	97.5	5.1	410	2	AB0077	proba	otran
59	97	5.1	493	2	T04446	hypot	prote
60	97	5.1	873	2	T12535	hypot	prote
61	95.5	5.0	950	2	D81821	glyci	rosen
62	95.5	5.0	1447	2	T42628	neuro	losis
63	93.5	4.9	369	2	A75091	ate h	ate h
64	93.5	4.9	1916	2	S46157	phosp	RIPI
65	93	4.9	319	2	A11526	hypot	- yea
66	92.5	4.8	379	2	A69516	hypot	prote
67	92	4.8	436	2	H70135	proba	rtate
68	91.5	4.8	329	1	A39440	flage	cltic
69	91.5	4.8	353	2	E91169	aspar	(EC 3
70	91.5	4.8	560	2	AB2437	chylt	proba
71	91	4.8	197	2	AD2613	NADH	enase
72	91	4.8	197	2	B97395	metly	rase
73	91	4.8	679	2	S46939	phosp	N-met
74	90	4.7	745	2	B84673	hypot	prote
75	89.5	4.7	357	2	E83205	hypot	prote
76	89	4.6	244	2	F70072	conse	othet
77	89	4.6	368	2	G86427	proba	ate 1
78	89	4.6	384	2	S73122	catba	sphat
79	89	4.6	488	2	T09734	proba	ropan
80	89	4.6	1620	2	I51339	1-amt	mpone
81	88.5	4.6	494	2	AD3255	comp1	1-for
82	88	4.6	524	2	G86834	ydrog	ydrog
83	87.5	4.6	556	1	A28185	alpha	(EC
84	87	4.5	1434	2	B36793	forma	hydro
85	86.5	4.5	351	2	B82496	hypot	prote
86	86.5	4.5	405	2	H71620	immun	rotei
87	86.5	4.5	421	2	C71893	aspar	nsam1
88	86.5	4.5	436	2	F69354	hydro	hydro
89	86	4.5	295	2	AC3276	TRK P	upca
90	86	4.5	319	2	AG1169	methy	rase
91	86	4.5	446	2	AD0861	hypot	prote
92	86	4.5	718	2	F90512	glyca	prote
93	85.5	4.5	205	2	C75155	hypot	prote
94	85.5	4.5	421	2	S45349	mechl	ta-la
95	85.5	4.5	292	2	F64622	l1 me	hydro
96	85.5	4.5	448	2	G87482	homos	riboxy
97	85.5	4.5	462	1	S29503	acetyl	multl
98	85.5	4.5	862	2	B36786	hypot	prote
99	85	4.4	255	2	G97227	prote	ining
100	85	4.4	306	2	A72610	prote	prote

ALIGNMENTS

RESULT 1

S18568
Lignin-bispecific O-methyltransferase (EC 2.1.1.-) - quaking aspen
N:Contains: 5-hydroxyferulic acid O5-methyltransferase (EC 2.1.1.-); caffeate O-methyltr
C:Species: Populus tremuloides (quaking aspen)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
R:Bugos, R.C.; Chiang, V.L.C.; Campbell, W.H.
Plant Mol. Biol. 17, 1203-1215, 1991
A>Title: cDNA cloning, sequence analysis and seasonal expression of lignin-bispecific ca
A:Reference number: S18568; MUID:92032785; PMID:1932694
A:Accession: S18568
A:Molecule type: mRNA

A:Residues: 1-365 <BUG>
A:Cross-references: UNIPROT:Q00763; UNIPARC:UPI0000127EA8; EMBL:X62096; NID:G20950; PIDN
A>Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 63-Ser
A:Accession: S40017

A:Molecule type: protein
A:Residues: 165-184,335-346;349-359 <BD2>
A:Cross-references: UNIPARC:UPI00000A8C65; UNIPARC:UPI0000178C30; UNIPARC:UPI0000178C31
R:Bugos, R.C.; Chiang, V.L.; Campbell, W.H.
Phytochemistry 31, 1495-1498, 1992

A>Title: Characterization of bispecific caffeic acid/5-hydroxyferulic acid O-methyltrans
A:Reference number: A56669; MUID:92344802; PMID:1368360
A:Accession: A56669

A:Status: preliminary
A:Molecule type: protein
A:Residues: 165-184,335-346;349-359 <BDW>
A:Cross-references: UNIPARC:UPI00000A8C65; UNIPARC:UPI0000178C30; UNIPARC:UPI0000178C31
A>Note: sequence modified after extraction from NCBI backbone
C:Superfamily: O-methyltransferase

C:Keywords: blocked amino end; lignin biosynthesis; methyltransferase; S-adenosylmethion

Query Match 83.3%; Score 1595.5; DB 2; Length 365;

Best Local Similarity 80.9%; Pred. No. 2.6e-123;

Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;

QY 1 MGSSTETKSPSEBAAAEEBAFVPMOLTSASVLPMTLSAIELDVLEIMAKAGPAGATIS 60
DB 1 MGSSTETQMTPTQ--VSDEEAMLFAMQLASASVLPMTLTAIELDLEIMAKAGPAGATIS 58
QY 61 TSDIASKLPPTKMPDAVMDRLMLRLASVYLTCSLRTLPDGKIEBLYGLAVCKFLTN 120
DB 59 TSEIASHLPTKMPDAVMDRLMLRLASVYLTCSLKDLPDGKVERLYGLAVCKFLTN 118
QY 121 DDGVSIALSLNODKVLMSWYHLTEAVLEGIPFNKAYGWTAFEGHGTDPRTVFNPN 180
DB 119 EDGVSISPLCLNMDKVLMSWYLLKDALIDGIPFNKAYGWTAFEGHGTDPRTVFNPN 178
QY 181 GMSNSTITMKKILETYKGFEGLGSVVDVGGTGAAHLMITAKYPMIKGINFDLPHVIEE 240
DB 179 GMSDSTITMKKILETYKGFEGLTSLVDVGGTGAAVNTIVSKYPSIKGINFDLPHVID 238
QY 241 APSYGEVHVGGDMFVSYPKGDALFMKMICHDMSDEHCKLFLKCYEALPTNGKYLAE 300
DB 239 APSYGEVHVGGDMFVSYPKADAVFMKMICHDMSDEHCKLFLKNCYCDALPENGKYLAE 298
QY 301 ILPVPADSLPTKAVVHIDVIMLAHNPCKERTKEFEALAGAGPGRVVAACAINT 360
DB 299 ILPVPADSLPTKAVVHIDVIMLAHNPCKERTKEFEALAGAGPGRVVAACAINT 357
QY 361 IIEFLKK 367
DB 358 IIEFLKK 364

RESULT 2

T09673
caffeate O-methyltransferase (EC 2.1.1.68) - alfalfa
C:Species: Medicago sativa (alfalfa)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 1
C:Accession: T09673

R:Gowri, G.; Bugos, R.C.; Campbell, W.H.; Maxwell, C.A.; Dixon, J
Plant Physiol. 97, 7-14, 1991

A>Title: Molecular cloning and expression of alfalfa S-adenosyl-)
A:Reference number: Z16815

A:Accession: T09673

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-365 <GOW>
A:Cross-references: UNIPROT:P28002; UNIPARC:UPI00000433FC; EMBL:J
A:Experimental source: subspecies sativa, cultivar Apollo

C:Function:
A:Pathway: Lignin biosynthesis
C:Superfamily: O-methyltransferase

C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 80.7%; Score 1544.5; DB 2; Length 365

Best Local Similarity 78.8%; Pred. No. 4e-119;

Matches 290; Conservative 42; Mismatches 33; Indels 2;

QY 1 MGSSTETKSPSEBAAAEEBAFVPMOLTSASVLPMTLSAIELDVLEIM 60
DB 1 MGSSTETQITPTH--ISDEEAMLFAMQLASASVLPMTLKSALIEDLLEIT 58
QY 61 TSDIASKLPPTKMPDAVMDRLMLRLASVYLTCSLRTLPDGKIEBLYGL 120
DB 59 PREIASQLPTNPDAVMDRLMLRLACIILITCSVRRQDGKVRVLGL 118
QY 121 DDGVSIALSLNODKVLMSWYHLTEAVLEGIPFNKAYGWTAFEGHGT 180
DB 119 EDGVSIALSLNMDKVLMSWYHLKDALIDGIPFNKAYGWTAFEGHGT 178
QY 181 GMSNSTITMKKILETYKGFEGLGSVVDVGGTGAAHLMITAKYPMIGII 240
DB 179 GMSDSTITMKKILETYKGFEGLKSLVDVGGTGAVNTIVSKYPTLGIN 238
QY 241 APSYGEVHVGGDMFVSYPKGDALFMKMICHDMSDEHCKLFLKCYEALP 300
DB 239 APSYGEVHVGGDMFVSYPKADAVFMKMICHDMSDEHCKLFLKCYEALP 298
QY 301 ILPVPADSLPTKAVVHIDVIMLAHNPCKERTKEFEALAGAGPGRV 360
DB 299 ILPVPADSLPTKAVVHIDVIMLAHNPCKERTKEFEALAGAGPGRV 357
QY 361 IIEFLKKI 368
DB 358 IIEFLKKV 365

RESULT 3

S40146
catechol O-methyltransferase (EC 2.1.1.6) - cider tree

C:Species: Eucalyptus gunnii (cider tree)

C>Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 1
C:Accession: S40146

R:Grima-Petrenati, J.; Poeydomege, O.; Boudet, A.M.
submitted to the EMBL Data Library, August 1993

A:Reference number: S40146

A:Accession: S40146

A:Molecule type: mRNA

A:Residues: 1-366 <GR1>
A:Cross-references: UNIPROT:P46484; UNIPARC:UPI0000127EA5; EMBL:J

C:Superfamily: O-methyltransferase
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 80.2%; Score 1535; DB 2; Length 366

Best Local Similarity 78.2%; Pred. No. 2.4e-118;

Matches 287; Conservative 45; Mismatches 31; Indels 3;

QY 1 MGSSTETKSPSEBAAAEEBAFVPMOLTSASVLPMTLSAIELDVLEIT 60
DB 1 MGSSTETQMTPTQ--VSDEEAMLFAMQLASASVLPMTLSAIELDLEIT 58

104

line: caffeic aci

IID:G166419; PID:

1 2;

1: 60
2: 58
3: 120
4: 118
5: 180
6: 178
7: 240
8: 238
9: 300
10: 298
11: 360
12: 357

104

IID:G437776; PID:

1 3;

11 59
12 58

```

Qy 60 STSDIASLKLPTKNPDPAVMLDMRLRLASVYLTCSLRTLPGDKIERLYGLAVCEKFLR 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 SPGEAAQLPTQNPBPAPVMDLRI FRLLASYSVLTCTLRNLPDGKVERLYGLAPVCEKFLYK 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 120 NDDGVSIALLSINDDKVLMESSWYHLTEAVLEGGIFPNKAYYGMTAFHYTGTDPRFNTVEN 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 NEDGVSIALLNINDDKILMESWYLYKDAVLGGGIFPNKAYYGMTAFHYTGTDPRFKIFN 178
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 180 NGMSHSTITMKKIETETYGFEGLGVDDVGSGTAHLNMTIATYPMIGINDELPHVIE 239
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 RGMSSHSTITMKKIETETYGFEGLLEVDDVGSGTAVLSMTIAKTPSMKGINDELPHVIE 238
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 240 EAPSYPGVEHVGDMFVSPKGDALFMKVI CHDMSDEHCLKFKKCYEALPTNGKYLAE 299
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 DAPPLPGVGVHVGDMFVSPKGDALFMKVI CHDMSDHCIAKFLKNCYDALLPNIGKYLVAE 298
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 300 CILPAPADASLETKAVVHIDVIMLAHNPCKERTKEFEALAKGAGFEGFRVVASCAVNT 359
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 CVLPVYPDTLSLATKAVIHIDCIMLAHNPCKERTQKEFEFLAKGAGFQGQVWC -CAFGH 357
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 360 WIEEFK 366
      : : : : :
Db 358 HWMEFLK 364
      : : : : :

```

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RESULT 4
T12259
O-diphenol-O-methyltransferase (EC 2.1.1.-) - pepper
C/Species: Capsicum annuum (pepper)
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-Jan-2000
C/Accession: T12259
J/Lee, B.; Choi, D.; Lee, K.W.
U. Plant Biol. 41, 9-14, 1998
A>Title: Isolation and characterization of o-diphenol-O-methyltransferase cDNA clone in
A/Reference number: Z17476
A/Accession: T12259
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-359 <LE>
A/Cross-references: UNIPARC:UPI00000ABB7A; EMBL:U83789; NID:g1791351; PID:g1791352
A/Experimental source: very young green fruit
A/Superfamily: O-methyltransferase
C/Keywords: methyltransferase

Query Match          79.8%; Score 1527.5; DB 2; Length 359;
Best Local Similarity 77.9%; Pred. No. 9.8e-118;
Matches 285; Conservative 35; Mismatches 39; Indels 7; Gaps 2;

QY      1 MGSTSETMGSSSBAAAEEFAVFPMOLTSASVLPMLVLSAEILDVLVEIMARGGCAHS 60
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1 MDSTNQ-----NLQTDEAPLFAMQDASAVLPWLKSALEDLLETMAAGGAALS 54
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      61 TSDIASKLPTKNPDAAVMLDRLRLIASYVLTCSLRTPDGKIERLYGLAPVCFLTRN 120
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       55 PSELAQAQPTKNPEARPVWLDRLRLATYSVANCRLRTLPGSRVERLYSLAPVCCLITRN 114
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      121 DDGVSIALSLMNDQKVLMESSHYLTEAVLBEGIFPNKAYGMTAFYHGTDRFNTVPNN 180
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       115 ADGVSVAPLLLMNDQKVLMESSMYHLTDVAVLDDGVFPFNKAYGMTAFYHGTDPRFNKVENR 174
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      181 GMSNSHTITMKKIETTYKGFGIGSVVDVGGSCTGSHLMNIITAKYMIGINDLPHVLEE 240
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       175 GMSHSHTITMKKILEDYGFGBLNSIVDVGGTGTVNMNIYSKPSINGINFDLSHVIED 234
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      241 APSYPGEVHGDMFVSPKGDALFMKWI CHDWSDEHCILPKCKCYEALPTNGKYIILBC 300
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       235 APAYPGEVHGDMFVSPKADALFMKWI CHDWSDEHCILPKCKCYEALPAANGKYLVAEC 294
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      301 ILPPAPDAASLETKKAVMHIDVTMLANPBGKERTKEFEPLAKAGAFBGRVVASCAVNTW 360
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       295 ILPETPDTSAATKNAVHDIVLMLANPBGKERTKEFEPLAKAGAFGTFR-RACCAVOTW 353
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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QY	361	11EFLK	366
		:::	
Db	354	VMEFHK	359

```

RESULT 5
T09780
Probable caffeate O-methyltransferase (EC 2.1.1.68) G2 - quaking
C1Species: Populus tremuloides (quaking aspen)
C1Date: 16-Jul-1999 #sequence_16-Jul-1999 #next_change
C1Accession: T09780
R1Hu: W.J.

```

submitted to the EMBL Data Library, March 1996

A:Reference number: Z16849

A:Accession: J09780

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-364 <H1U>

A:Cross-references: UNIPROT:Q41086; UNIPARC:UPI000009D55C; EMBL:

A:Experimental source: strain Mchx

C:Genetics:

A:Gene: OMTG2

C:introns: 139/2; 243/1; 264/3

C:Superfamily: O-methyltransferase

C:Keywords: l1gln biosynthesis; methyltransferase; S-adenosylmeth

Query Match 78.9%; Score 1510; DB 2; Length 364

Best local Similarity 77.9%; Pred. No. 2.7e-116;

Matches 286; Conservative 38; Mismatches 39; Indels

Qy	1	MGSTSETKMSPEBAAAABEEAFVFAMQLTSASVLPMLKSAIBDVLEIM	IS 60
Db	1	MSGTGETQMS--AQIDBEEA-NFALQLISSSVLPMLUKTAIBDLEIM	LP 57
Qy	61	TSDIASKLPTKPNDAAVMLDRMLRLIASYSVLTCSRLTPDGKIERLYGL	RN 120
Db	58	PSDIASHLPTKPNPAPVYMLDRITLRILIASYSLTICSLRPLPGKTERLYGL	RN 117
Qy	121	DGVSIALIASLNQDKVIMESWYHLTEAVLEGGIPFNKAYGMTAFBYHGT	NN 180
Db	118	EDGVSVSPCLNQDKVIMESWYHLKDALIEGGIPFNKAYGMTAFBYHGT	NK 177
Qy	181	GMSNHSSTIMKKILLETYKFGBSGVVDVGGGTGAHLMIITAKYPMIKGI	EE 240
Db	178	GMSVHSKMAKKILLETYKFGBSIASLVVDGGGTAVVSTIVSKYPSIKGI	AD 237
Qy	241	ABSYRGVEHYGDMVSPVKGDALIMKRICHDMSDEHCKATLKCYALP	EC 300
Db	238	APAFPGVEHYGDMFVSVPKADAVPMKVICHDMSDEHCTFLKNCYALP	EC 297
Qy	301	ILPVAPDASLPKCAVYHIDVIMLANPGSKRTERKEPEALAKGCFPGFR	TW 360
Db	298	ILPVADTSLATKGVMHVDVIMLANPGSKERTDREFESLARAGCFGFE	TH 356
Qy	361	ITIEFLKK 367	
Db	357	VIEFRKK 363	

RESULT 6
S36403
cathchol O-methyltransferase (EC 2.1.1.6) - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 004
C/Accession: S36403
R/Legrand, M.
submitted to the EMBL Data Library, August 1993
A/Reference number: S36403
A/Accession: S36403
A/Molecule type: mRNA
A/Residues: 1-364 <LBS>
A/Cross-references: UNIPROT:Q42958, UNIPARC:UPI000002D50B, EMBL:
A/Superfamily: O-methyltransferase
NID:g396588, PID

C.Keywords: methyltransferase; S-adenosylmethionine

Query Match 78.3%; Score 1499.5; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 2e-115;
Matches 281; Conservative 36; Mismatches 41; Indels 3; Gaps 2;

QY 1 MGSTSETKMSPEBAALAEAEAFVFAAQQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 60
DB 1 MGSTSETKMSPEBAALAEAEAFVFAAQQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 58
QY 61 TSDIASKLPTKNDPAVMDRLMLRLASVLTCSLRTLPDGIKIERLYGLAPVCKFLPTN 120
DB 59 PSELAAQSLSTQNPBAVMDRLMLRLASVLTCSLRTLPDGIKIERLYGLAPVCKFLPTN 118
QY 121 DDGVSIALSLNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEHGTDRFNTVFN 180
DB 119 ADGVSAPRLLLNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEHGTDRFNTVFN 178
QY 181 GMSNSTITMKKILLEYKGFEGISVVDVGGGGAHLNMIITAKYPMIKGINFDLPVIEE 240
DB 179 GMSDSTMSMKKILLEYKGFEGISVVDVGGGGAHLNMIITAKYPMIKGINFDLPVIEE 238
QY 241 ABSYGVHEVGDMPFVSPKDAIFPMKWI CHDMSDEHCLKFKCYEALPTNGKYLAE 300
DB 239 AFTYGVHEVGDMPFVSPKDAIFPMKWI CHDMSDEHCLKFKCYEALPTNGKYLAE 298
QY 301 ILPVAPDASLPTRKAVVHIDVIMLANHPGKERTKEFEALAGAGPFGF-RVVASCAVNT 359
DB 299 ILPEAPDTSLATKNTVHVIDVIMLANHPGKERTKEFEALAGAGPFGFRLVALTLTGS 358
QY 360 W 360
DB 359 W 359

RESULT 7
S36404
catechol O-methyltransferase (EC 2.1.1.6) - common tobacco
C/Species: Nicotiana tabacum (Common tobacco)
C/Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S36404
R/Legrand, M.
submitted to the EMBL Data Library, August 1993
A/Reference number: S36403
A/Accession: S36404
A/Molecule type: mRNA
A/Residues: 1-364 <LEG>
A/Cross-references: UNIPROT:Q04065; UNIPARC:UP100000ACF72; EMBL:X74453; NID:G396590; PII
C/Superfamily: O-methyltransferase
C/Keywords: methyltransferase; S-adenosylmethionine

Query Match 77.5%; Score 1484.5; DB 2; Length 364;
Best Local Similarity 77.0%; Pred. No. 3.4e-114;
Matches 278; Conservative 38; Mismatches 42; Indels 3; Gaps 2;
QY 1 MGSTSETKMSPEBAALAEAEAFVFAAQQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 60
DB 1 MGSTSETKMSPEBAALAEAEAFVFAAQQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 58
QY 61 TSDIASKLPTKNDPAVMDRLMLRLASVLTCSLRTLPDGIKIERLYGLAPVCKFLPTN 120
DB 59 PSELAAQSLSTQNPBAVMDRLMLRLASVLTCSLRTLPDGIKIERLYGLAPVCKFLPTN 118
QY 121 DDGVSIALSLNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEHGTDRFNTVFN 180
DB 119 ADGVSAPRLLLNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEHGTDRFNTVFN 178
QY 181 GMSNSTITMKKILLEYKGFEGISVVDVGGGGAHLNMIITAKYPMIKGINFDLPVIEE 240
DB 179 GMSDSTMSMKKILLEYKGFEGISVVDVGGGGAHLNMIITAKYPMIKGINFDLPVIEE 238
QY 241 ABSYGVHEVGDMPFVSPKDAIFPMKWI CHDMSDEHCLKFKCYEALPTNGKYLAE 300
DB 239 AFTYGVHEVGDMPFVSPKDAIFPMKWI CHDMSDEHCLKFKCYEALPTNGKYLAE 298

DB 239 APAYGVHEVGDMPFVSPKDAIFPMKWI CHDMSDEHCLKFKCYEALP 300
QY 301 ILPVAPDASLPTRKAVVHIDVIMLANHPGKERTKEFEALAGAGPFGF-RVVASCAVNT 359
DB 299 ILPEAPDTSLATKNTVHVIDVIMLANHPGKERTKEFEALAGAGPFGF 358
QY 360 W 360
DB 359 W 359

RESULT 8
T12260
caffeoyl-CoA O-methyltransferase (EC 2.1.1.104) - common ice plant
C/Species: Mesembryanthemum crystallinum (Common ice plant)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 1
C/Accession: T12260
R/Michaelowski, C.B.; Bohnert, H.J.
submitted to the EMBL Data Library, March 1998
A/Description: Mesembryanthemum crystallinum caffeic acid 3-O-methyltransferase.
A/Reference number: Z17477
A/Accession: T12260
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-350 <MIC>
A/Cross-references: UNIPROT:O65362; UNIPARC:UP100000A4A72; EMBL:J
C/Function: 11gnin biosynthesis
A/Pathway: 11gnin biosynthesis
C/Superfamily: O-methyltransferase
C/Keywords: methyltransferase; S-adenosylmethionine

Query Match 73.3%; Score 1403.5; DB 2; Length 359;
Best Local Similarity 74.6%; Pred. No. 1.5e-107;
Matches 261; Conservative 46; Mismatches 42; Indels 1;
QY 18 EBEAFVFAAQQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHISDIAK 177
DB 1 EBEACSYAMTITSGSVPMVWLKAVIELDVLEIKRAGPQAQLSPAIAAQ 176
QY 78 MIDRLMLRLASVLTCSLRTLPDGIKIERLYGLAPVCKFLPTNDGVSIA 137
DB 61 MIDRLMLRLASVLTCSLRTLPDGIKIERLYGLAPVCKFLPTNDGVSIA 120
QY 138 IMESWYHLTEAVLEGIPFNKAYGWTAFEHGTDRFNTVFNNGMSNST 197
DB 121 IMESWYHLTEAVLEGIPFNKAYGWTAFEHGTDRFNTVFNNGMSNST 180
QY 198 KGFEGISVVDVGGGGAHLNMIITAKYPMIKGINFDLPVIEEAPSPGV 257
DB 181 KGFEGISVVDVGGGGAHLNMIITAKYPMIKGINFDLPVIEEAPSPGV 240
QY 258 VPKGDAIFPMKWI CHDMSDEHCLKFKCYEALPTNGKYLAECLIPVAD 317
DB 241 VPKGDAIFPMKWI CHDMSDEHCLKFKCYEALPTNGKYLAECLIPVAD 300

QY 318 IDVIMLANHPGKERTKEFEALAGAGPFGF-RVVASCAVNTIIEFLK 300
DB 301 VDAILMLANHPGKERTKEFEALAGAGPFGF-RVVASCAVNTIIEFLK 299
RESULT 9
S28612
catechol O-methyltransferase (EC 2.1.1.6) - maize
C/Species: Zea mays (maize)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 1
C/Accession: S28612
R/Collazo, P.; Montoliu, L.; Puigdomenech, P.; Rigau, J.
Plant Mol. Biol. 20, 857-867, 1992
A/Title: Structure and expression of the 11gnin O-methyltransferase
A/Reference number: S28612; MUID:93099238; PMID:1463825
A/Accession: S28612
A/Molecule type: DNA
A/Residues: 1-364 <COL>
from Zea mays L.

A:Cross-references: UNIPROT:Q06509, UNIPARC:UPI0000127EA6; EMBL:M73235; NID:g1256711; P1
A:introns: 141/2
A:Superfamily: O-methyltransferase
C:Keywords: methyltransferase; S-adenosylmethionine
Query Match 61.9%; Score 1185; DB 2; Length 364;
Best Local Similarity 61.8%; Pred. No. 1,4e-89;
Matches 230; Conservative 51; Mismatches 77; Indels 14; Gaps 7;
OY 1 MGSTSEKMSPESEAAAEBAFVPMOLTSASVLPVMTKSAIELDVLEIMAK-AGPG-AH 58
DB 1 MGST-----AGDVAADVDEECWYAMQASSIIPMTLKNALIEGLILEVLOEAGGKAA 55
OY 59 ISTDIAASKLPTKND--DAVMDRLMLRLASVLTCTSLTPDPGKIERLYGLAPVK 115
DB 56 LAEEVVAHPAAPSDEPAALAAVMDRLMLRLASVTVRCQMED-RDGRYERYSAAPVK 114
OY 116 FLTRNDGVSIALSLNQDQVLMESWYHLTEAVLEGGIPFKAYGMTAFEYHGTDPEN 175
DB 115 WLTPNEGVSMAALANMODVLMESWYTLXDAVLVDGGIPFKAYGMTAFEYHGTDPEN 174
OY 176 TVNNNGSNSTITMKKILERTYKGPBGSGVVDGSGGTHANMIIAKPMIKGTFDIP 235
DB 175 RVFNEGKNSVITTKLLDPTTGPBGVSTLDVGSGVATLHAITSRPHISGVNFDIP 234
OY 236 HVIEBAPYPGEVHEVGDMPFVSPKGDAPFMKMLCHDMSDEHCLFLKCYEALPTNGKY 295
DB 235 HVISEAPPPGVHNVGDMFASVPAGDAIIMKMLHDMSDMCAITLKNCTDALPENGKY 294
OY 296 ILAECTLPVADSLPTKAVVHIDVIMLANNPGKERTKEFEALAKGAFEGFRVASC 355
DB 295 IVECVLPVTEATPKAQGVHVDIMLANNPGKERYERERELAKGAFSGFK--ATY 352
OY 356 AY-NTWIIIEFLK 366
DB 353 IYANAWAIEFIK 364
RESULT 10
JO2344
catechol O-methyltransferase (EC 2.1.1.6) III - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: JO2344; PQ0814
R:Allele: L.; Geoffroy, P.; Fritig, B.; Legend, M.
Plant Physiol. 103, 509-517, 1993
A:Title: Molecular cloning and expression of a new class of ortho-diphenol-O-methyltrans-
A:Reference number: JO2344; MUID:94302149; PMID:7518088
A:Accession: JO2344
A:Molecule type: mRNA
A:Residues: 1-365 <PEL1>
A:Cross-references: UNIPROT:Q42949; UNIPARC:UPI00000ACDD; EMBL:X71430; NID:g429113; P1D
A:Accession: PQ0814
A:Molecule type: protein
A:Residues: 8-33;55-61;106-114;136-145;161-169;175-180;181-191;193-198;199-204;205-218;2
A:Cross-references: UNIPARC:UPI0000178C32; UNIPARC:UPI0000178C33; UNIPARC:UPI0000178C34;
C39; UNIPARC:UPI0000178C3A; UNIPARC:UPI0000178C3B; UNIPARC:UPI0000178C3C; UNIPARC:UPI000
A:Experimental source: leaf, cv. Samsum NN
C:Gene: OMT
C:Species: A:Gene: OMT
C:Superfamily: O-methyltransferase
C:Keywords: methyltransferase; S-adenosylmethionine
Query Match 55.5%; Score 1062.5; DB 2; Length 365;
Best Local Similarity 57.6%; Pred. No. 1.6e-79;
Matches 212; Conservative 51; Mismatches 94; Indels 11; Gaps 7;
OY 5 SETKMSPESEAAAEBAFVPMOLTSASVLPVMTKSAIELDVLEIMAKGPAHISTDI 64
DB 3 SSTK-SQIPQSEEBRNCTYAMQLSSVLPVHSTIQLEVEFELAKSN-DTKASASOI 60
OY 65 ASKLPK-KNPDAVMDRLMLRLASVLTCTSLTPD---GKIERLYGLAPVKFLTR 119

[illegible]

Db 317 LDCHLVNNGGKSKEDFELASKSTGYDVLC-CAYDWMELYKX 365

RESULT 12

T09617
Isoiquiritigenin 2'-O-methyltransferase - alfalfa
C:Species: Medicago sativa (alfalfa)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #next_change 09-Jul-2004
C:Accession: T09617
R:Maxwell, C.A.; Harrison, M.J.; Dixon, R.A.
Plant J. 4, 971-981, 1993
A:Title: Molecular characterization and expression of alfalfa isoiquiritigenin 2'-O-methyltransferase.
A:Reference number: Z16778; MUID:94108491; PMID:8281189
A:Accession: T09617
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-372 <MAX>
A:Cross-references: UNIPROT:P93324; UNIPARC:UPI000000A3969; EMBL:LI0211; NID:g289126; PID A:Experimental source: subspecies sativa; cultivar Apollo
C:Function:
A:Description: methylates the 2'-hydroxyl of isoiquiritigenin (2',4',4'-trihydroxychalcone)
A:Note: 4,4'-dihydroxy-2'-methoxychalcone is the most potent of the nod-gene-inducing flavonoids
C:Superfamily: O-methyltransferase
C:Keywords: methyltransferase

Query Match 43.7%; Score 836; DB 2; Length 372;
Best Local Similarity 46.9%; Pred. No. 6,7e-61;
Matches 175; Conservative 71; Mismatches 119; Indels 8; Gaps 5;

QY 1 MGS---TSETKSPSEAAAEAFVFAVQLTSAVLPWVLSKATLELDVLEIMAKP-GRG 56
DB 1 MGNSTTKEDNDQISATSEGTEDSACLSAMVLTNNLVYPAVNAALDNLFEIIAAKTPRG 60
QY 57 AHISTSDIASKP--TKNDAAVMDRLRLILASYSVLTCSLRTLPDGKIERLYGLAPVC 114
DB 61 AFMSSEIASKLPASTQSHDLFNRDLRMLRLASYSVLTSTRRTIEDGAEKRVYGLSMVG 120
QY 115 KFLTRNDGCVSLAALSLNQDKVLMESWHLTEAVLEGGIP-FNKAYGMTAEFHYGTDPK 173
DB 121 KVLVDESKGYLASFETPLCYPALLLQVMMNFKFAVDEDDIDLFKNVHGVTKEFNGKCK 180
QY 174 FVTVFNNGSNSTITMKKILFTYKGFEGSLGVVDVGGTGAHLMVIAKYPMIGIND 233
DB 181 MNOIRKSNVDCATKEMKMLKLEIYTGEGISTLVVGGSGKNLEILLISKYPLKGINFD 240
QY 234 LPHVIEASPSYGVHVGDMFVSPKDAIPMKWICHMSDEHCLKFLKCYEALPTNG 293
DB 241 LPOVIENAPPLSGIEHVGDMFASVQGDAMITLKAVCHMSDEKCIIEFLSNCHKALSPNG 300
QY 294 KYTLAECLIPVADSLPTKAVVHIDVIMLAINPGKERTKEFEFLAAGAFEGPRVYA 353
DB 301 KYIIVFELIPBPNNSESKLVSTLDNMF1-TVGGRERTKQYKLSLGSFKFQVAC 359
QY 354 SCAYNTWIEFLK 366
DB 360 RAFNSLGVMEFYK 372

RESULT 13

E96559
hypoethetical protein P5F19.5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #next_change 09-Jul-2004
C:Accession: E96559
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: E96559
A:Status: preliminary
A:Accession: E96559
A:Molecule type: DNA
A:Residues: 1-363 <STO>
A:Cross-references: UNIPROT:Q9ZU24; UNIPARC:UPI0000048381; GB:AEI
C:Superfamily: O-methyltransferase

Query Match 43.4%; Score 832; DB 2; Length 363;
Best Local Similarity 47.3%; Pred. No. 1.4e-60;
Matches 168; Conservative 64; Mismatches 119; Indels 4;

QY 12 SEAAAEAEAFVFAVQLTSAVLPWVLSKATLELDVLEIMAKP-GAHIS 70
DB 6 TSGGSEEDMLAIQGLNFPVYIVTARELDLFEIMAKRPLGSLYSI 65
QY 71 KNPDAAVMDRLRLILASYSVLTCSLRTLPDGKIERLYGLAPVCFLTRNI 130
DB 66 KNFAPPMIDRLRPLVAVSVCTKLVDEGRSRAVGLGVGKLLKDI 125
QY 131 LMNDKVLMESSMYHLTEAVLEGGI-FNKAYGMTAEFHYGTDPK 189
DB 126 LAGCTKAGVWSYVTEALIQGASAWERABALIFEMKKNENLKLFNI 185
QY 190 MKKILETKYKGFEGSLGVVDVGGTGAHLMVIAKYPMIGINDPLVHIEI 249
DB 186 MKKILENVIKGFEGVSDPVDVGGSLGSLNLAQLLSKYPHILKGINFDLPHTVK 245
QY 250 VGDMPFVSPKGDALPMKWIHMSDEHCLKFLKCYEALPTNGKVIYLA 308
DB 246 IGGDMFDEIPRGEVILMKWILHMDNDEKCVBILKNCKKALPBTGRIYIEI 305
QY 309 SLPTKAVVHIDVIMLAINPGKERTKEFEFLAKAGFEGPRVVASCAVN 308
DB 306 DLATKNSLSADLTWMSLTSGGKERTKEFEFLAKAGFKLPKTIYV -AYS 305

RESULT 14

E96804
hypoethetical protein TSM16.12 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #next_change 09-Jul-2004
C:Accession: E96804
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: E96804
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-381 <STO>
A:Cross-references: UNIPROT:Q9CAQ3; UNIPARC:UPI0000048442; GB:AEI
C:Superfamily: O-methyltransferase

Query Match 43.4%; Score 831.5; DB 2; Length 38;
Best Local Similarity 45.6%; Pred. No. 1.6e-60;
Matches 171; Conservative 72; Mismatches 113; Indels 3;

un, H.; Tallon, I

ID:g4220447; PII

4;

70

65

130

125

189

185

249

245

308

305

3

te, O.; Alonso, C.H.; Dewar, K.;

104

sin, E.; Kim, C.C.

-, R.; Marziani, R.;

un, H.; Tallon, I

ID:g6382500; PII

Qy	2	GS7SETKMSPEEAAAABEEAEVFPAMQLTSASVLPVUKSAILEDYLTBEIMARAGCAHIST	61
Db	16	GLTIEEGIDEEKMVSLOAHESTIV-----NAAPFVVILKALLEGVITDITLAASNGTWLSP	69
Qy	62	SDIASKLPTK--NPDAVMILDRMLRLTLASVEVLTC---SLRTPDPGKIERLYGLAPVCK	115
Db	70	SEIAVSLPNKRTNTEAPVLDLRMLRLVSHSLIKCCMWESRENGOTGKIERVYAAEPCK	129
Qy	116	PLTENDGV-SIALSLMNODKVLMEHWYHLTEAVLEGGIDPNKAYGTAEFYHTDPRF	174
Db	130	YFLKDSGGSGSLSSLLLIHSHQVILKTTWNLKDVILEGKDAFPSSAHDRLEPEYISSDDQF	189
Qy	175	NTVNNNMNSNSTITMKKILLETYKGFEGLGSVDVVGCGTGAHLMNIIAKYPMIGINDL	234
Db	190	SKLPHRAMSESTTWMKKVLEERYGFEDVNTLVDVGGIGTILGLITSKYPIHIGVNDL	249
Qy	235	PHVIEAPSYEGVHVHVGDMFVSPKGDALFMKVICHDMSDEHCLFKPKCEYALPTGK	294
Db	250	AQVLTQAPFYGVGHVSGDMFIEVPKGDALITMKMIIHDMGSEDCKILIANCKMSLPEVKG	309
Qy	295	VIIAECILPVAP--DASLPTKAVVHIDVIMLAHNPGEKERTTEKEFEALAGACFEGERV	351
Db	310	VIIIVEMITPMKEPKNDPESCNT--VLGMDLMLTGCGSGGKERSLQFEBULAPASGFLCEI	367
Qy	352	VASCAVNTWIIIEFLK	366
Db	368	IC-LSYSYSVLEIEPHK	381

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 08:26:54 , Search time 230 Seconds
(without alignment)
1128.845 Million cell updates/sec

Title: US-10-681-878A-6
Perfect score: 1915
Sequence: 1 MGS1ETKMSPEAAAAAE.....PRVASCANTWTFELKKI 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniproct 05.80:*
1: uniproct_proct:*
2: uniproct_trendi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1894.5	98.9	367	09SMR0_L10ST	09SMR0 liquidambar
2	1602.5	83.7	365	1 COMT1_FRUDU	043609 prunus dulcis
3	1601.5	83.6	365	1 COMT1_ROSCH	089625 rosa chinensis
4	1595.5	83.3	365	1 COMT1_POPPM	000763 populus tremula
5	1595.5	83.3	365	2 07X9J0_ROSCH	07X9J0 rosa chinensis
6	1589.5	83.0	365	2 09M602_FRAN	09M602 fragaria ananassa
7	1588.5	83.0	365	1 COMT1_POPPM	043046 populus alba
8	1579.5	82.5	360	2 09M565_PROSI	09M565 populus tremula
9	1578.5	82.4	364	2 09LMB8_PROSI	09LMB8 populus tremula
10	1544.5	80.7	365	1 COMT1_MEDSA	09LMB8 medicago sativa
11	1535	80.2	366	1 COMT1_EUCUC	046484 eucalyptus globulus
12	1528	79.8	370	1 COMT1_CLABR	023760 clarkia borealis
13	1527.5	79.8	359	1 COMT1_CAPAN	09F4Y8 capsicum annuum
14	1523.5	79.6	361	1 COMT1_OCIBA	09XGW0 ocimum basilicum
15	1511	78.9	364	1 COMT2_POPIK	041086 populus tremula
16	1510	78.9	364	1 COMT2_POPIK	08W013 catharanthus roseus
17	1506.5	78.7	363	1 COMT1_CATRO	042958 nicotiana glauca
18	1499.5	78.3	364	2 042958_TOBAC	09XGV9 ocimum basilicum
19	1491.5	77.9	361	1 COMT2_OCIBA	09XGV9 ocimum basilicum
20	1484.5	77.5	364	2 004065_TOBAC	004065 nicotiana glauca
21	1483.5	77.5	350	1 COMT1_COPCA	081187 coffea arabica
22	1473.5	76.9	363	1 COMT1_ARATH	09F1K25 arabidopsis thaliana
23	1468.5	76.7	359	1 COMT1_CAPCH	081446 capsicum annuum
24	1460.5	76.3	365	2 06T1F5_GAPPA	06T1F5 gappa
25	1432	74.8	386	2 09M560_VITVI	09M560 vitis vinifera
26	1403.5	73.3	350	2 06S362_MESCR	06S362 mesembryanthemum
27	1401	73.2	362	2 09XK90_USRUD	09XK90 thalictrum flavum
28	1395	72.8	362	2 09XK92_USRUD	09XK92 thalictrum flavum
29	1395	72.8	362	2 09XK92_USRUD	09XK92 thalictrum flavum
30	1389	72.5	364	2 09SYR8_USRUD	09SYR8 thalictrum flavum
31	1387	72.4	343	1 OMT2_CHRAE	042653 chrysosplenium

32	1384	72.3	312	2	09SMC1_EUCGL	09SMC1	ptus
33	1384	72.3	364	2	09XK91_USRUD	09XK91	trum
34	1383	72.2	343	1	OMT1_CHRAE	P5904	splen
35	1341	70.0	368	1	1EMT1_CLABR	00438	a bre
36	1339	69.4	354	1	COMT1_ZINEL	04323	eleg
37	1266.5	66.1	360	2	06MUC0_PAPSO	06MUC0	r som
38	1266	65.1	313	1	COMT1_EUCGL	09SMC1	ptus
39	1246	65.1	360	2	094GA5_PESAR	094GA5	a aru
40	1244	65.0	360	2	094GB0_PESAR	094GB0	a aru
41	1241	64.8	360	2	022381_LOLPR	02238	pere
42	1239	64.7	360	2	084N28_WHEAT	084N28	um ae
43	1234	64.4	360	2	092TU2_LOLPR	092TU2	. pere
44	1234	64.4	360	2	092TU2_LOLPR	092TU2	rum o
45	1213	63.3	362	1	COMT1_SACOF	08205	rum o
46	1212.5	63.3	361	2	092TU0_LOLPR	092TU0	pere
47	1212	63.3	362	2	06UNM7_9POL	06UNM7	rum h
48	1208.5	63.1	365	2	05KSL8_IRIHO	05KSL8	ollan
49	1207	63.0	360	2	094GA7_PESAR	094GA7	a aru
50	1198	62.6	343	2	042654_CHRAE	04265	splen
51	1194	62.3	368	2	06ZD89_ORISA	06ZD89	ativ
52	1193	62.3	364	2	06VWF7_MAIZE	06VWF7	ys (m
53	1191.5	62.2	354	2	06T1F6_GAPPA	06T1F6	ajub.
54	1187	62.0	364	2	06VWF6_MAIZE	06VWF6	ys (m
55	1185	61.9	364	1	COMT1_MAIZE	06VWF6	ys (m
56	1185	61.9	364	2	06GLJ6_MAIZE	05GLJ6	ys (m
57	1184	61.8	364	2	06VWF3_MAIZE	06VWF3	ys (m
58	1184	61.8	364	2	06VWF2_MAIZE	06VWF2	ys (m
59	1172	61.2	358	2	06VWF2_MAIZE	06VWF2	ys (m
60	1164	60.8	358	2	06VWF6_MAIZE	06VWF6	ys (m
61	1164	60.8	359	2	06VWF6_MAIZE	06VWF6	ys (m
62	1164	60.8	359	2	06VWF6_MAIZE	06VWF6	ys (m
63	1163	60.7	359	2	06VWF3_MAIZE	06VWF3	ys (m
64	1163	60.7	359	2	06VWF3_MAIZE	06VWF3	ys (m
65	1163	60.7	359	2	06VWF2_MAIZE	06VWF2	ys (m
66	1162	60.7	358	2	06VWF1_MAIZE	06VWF1	ys (m
67	1152	60.2	362	2	084X55_SORBI	084X55	m bic
68	1147	59.9	362	2	08W215_SORBI	08W215	m bic
69	1142.5	59.7	371	2	06L8K4_ROSCH	06L8K4	hinen
70	1135	59.3	364	2	05NDD5_PICAB	05NDD5	abies
71	1090.5	56.9	365	2	06Q796_VANPL	06Q796	a pia
72	1064.5	55.6	364	2	06VMV9_MENPI	06VMV9	pide
73	1062.5	55.5	365	2	042949_TOBAC	042949	ana t
74	1059	55.3	292	2	070CS6_PESAR	070CS6	a aru
75	1047	54.7	365	1	1MT1_MESCR	P4598	tyanc
76	1046	54.6	292	2	070CS7_LOLMU	070CS7	mult
77	1037	54.2	364	2	08S3K6_TOBAC	08S3K6	ana t
78	978	51.1	351	2	092TU1_LOLPR	092TU1	Q863k
79	975	50.9	268	2	075W57_ORISA	075W57	Q87u5
80	948.5	49.5	352	2	08H0D1_HORVU	08H0D1	m vul
81	910	47.5	366	2	07X9J1_ROSCH	07X9J1	hinen
82	836	43.7	372	1	CHOMT1_MEDSA	P9332	go sa
83	832	43.4	363	2	09ZU24_ARATH	09ZU24	opsis
84	831.5	43.4	381	2	09CAQ4_ARATH	09CAQ4	opsis
85	830.5	43.4	381	2	09CAQ4_ARATH	09CAQ4	opsis
86	824.5	43.1	381	2	084WU8_ARATH	084WU8	opsis
87	824	43.0	367	2	096424_GLYEC	096424	opsis
88	817.5	42.7	338	2	08LAK3_ARATH	08LAK3	opsis
89	811.5	42.4	352	2	09WAP0_ARATH	09WAP0	opsis
90	805	42.0	201	2	071H66_WHEAT	071H66	um ae
91	803.5	42.0	373	2	09LPU8_ARATH	09LPU8	opsis
92	797	41.6	381	1	SMT1_COPUA	Q3352	opsis
93	794.5	41.5	373	2	09LPU5_ARATH	09LPU5	opsis
94	793.5	41.4	373	2	056XW7_ARATH	056XW7	opsis
95	790.5	41.3	373	2	08LGI0_ARATH	08LGI0	opsis
96	790.5	41.3	373	2	09LPU7_ARATH	09LPU7	opsis
97	789.5	41.2	373	2	09LPU6_ARATH	09LPU6	opsis
98	788	41.1	378	2	08L8L1_ARATH	08L8L1	opsis
99	787	41.1	378	2	09PHZ5_ARATH	09PHZ5	opsis
100	780.5	40.8	381	2	09CAM5_ARATH	09CAM5	opsis

ALIGNMENTS

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RESULT 1
Q9SKR0 LIQST PRELIMINARY; PRT; 367 AA.
ID Q9SKR0;
AC Q9SKR0;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DR 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
OS Caffeate O-methyltransferase (EC 2.1.1.6).
GN NameCOMT;
OS Liquidambar styraciflua (Amberboom) (Sweetgum tree).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Hamamelidaceae; Liquidambar.
OX NCBI_TaxID=4400;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Developing xylem;
RX MEDLINE=99362692; PubMed=10430877; DOI=10.1073/pnas.96.16.8955;
RA Osakebe K., Tsao C.C., Li L., Popko J.L., Umezawa T., Carraway D.T.,
RA Smeltzer R.H., Joshi C.P., Chiang V.L.;
RT "Conferyl aldohexose 5-hydroxylation and methylation direct syringyl
RT lignin biosynthesis in angiosperms."
RL Proc. Natl. Acad. Sci. U.S.A. 96:8955-8960(1999).
DR EMBL; AF139533; AAD48913.1; -, mRNA.
DR HSSP; P28002; 1KYZ.
DR SMR; Q9SKR0; 7-367.
DR GO; GO:0016206; F:catechol O-methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O Met trans2.
DR InterPro; IPR000051; SAM bind.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00891; Methyltransf_2; 1.
DR Methyltransferase; Transferase.
KW SEQUENCE 367 AA; 39970 MW; 3F05EB9BCB711779 CRC64;
SQ
Query Match 98.9%; Score 1894.5; DB 2; Length 367;
Best Local Similarity 99.5%; Pred. No. 1.9e-141;
Matches 366; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 MGSTSETKSPSEAAAEEBAFVFMQLTSASVLPVMTLSAIEDLVLEIMAKAGPGAHIS 60
DB 1 MGSTSETKSPSEAAAEEBAFVFMQLTSASVLPVMTLSAIEDLVLEIMAKAGPGAHIS 60
QY 61 TSDIASKLPTKNPDAVWMDRMLRLASYSVLTCSLRTPDGKIERLYGLAPVCKELTEN 120
DB 61 TSDIASKLPTKNPDAVWMDRMLRLASYSVLTCSLRTPDGKIERLYGLAPVCKELTEN 120
QY 121 DDGVSIAALSLNNQDQVLMESWYHLTEAVLEGGIPFNKAYGWTAFYHGTDPRFNTVFNN 180
DB 121 DDGVSIAALSLNNQDQVLMESWYHLTEAVLEGGIPFNKAYGWTAFYHGTDPRFNTVFNN 180
QY 181 GMSNHSITTMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIEE 240
DB 181 GMSNHSITTMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIEE 240
QY 241 AASYPEVEHVGGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCCYEALPTNGKYLAC 300
DB 241 AASYPEVEHVGGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCCYEALPTNGKYLAC 300
QY 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPGEGR-VALCAYNW 360
DB 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPGEGR-VALCAYNW 360
QY 361 IIEFLKKI 368
DB 361 IIEFLKKI 367
RESULT 2
COMT1_PRUDU STANDARD; PRT; 365 AA.
ID COMT1_PRUDU;
AC COMT1_PRUDU;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DR 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
OS Caffeate O-methyltransferase (EC 2.1.1.6).
GN NameCOMT1;
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus;
OX NCBI_TaxID=3755;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=cv. Texas; TISSUE=Root;
RA Garcia-Mas J., Messeguer R., Arus P., Puigdomenech P.;
RT "The caffeic acid O-methyltransferase from Prunus amygdalus
RT (ex) Plant Gene Register PGR95-006.
RL FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
RL and of 5-hydroxyferulic acid to sinapic acid. The result
RL products may subsequently be converted to the correspond
RL alcohols that are incorporated into lignins.
CC -1 CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-
CC cinnamate.
CC -1 PATHWAY: Lignin biosynthesis.
CC -1 SIMILARITY: Belongs to the methyltransferase superfamily;
CC family. COMT subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL
CC the European Bioinformatics Institute. There are no restrictions
CC use as long as its content is in no way modified and this statement
CC removed.
CC -----
DR EMBL; X83217; CAA58218.1; -, mRNA.
DR HSSP; P28002; 1KYZ.
DR SMR; Q43609; 5-364.
DR InterPro; IPR012967; Dimerisation.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O Met trans2.
DR InterPro; IPR000051; SAM bind.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF08100; Dimerisation; 1.
DR Pfam; PF00891; Methyltransferase; 2; 1.
DR Lignin biosynthesis; Methyltransferase; Transferase.
KW SEQUENCE 365 AA; 39762 MW; C8C4BFE7E0180E7 CRC64;
SQ
Query Match 83.7%; Score 1602.5; DB 1; Length 365;
Best Local Similarity 82.8%; Pred. No. 2.5e-118;
Matches 304; Conservative 31; Mismatches 29; Indels 1;
QY 1 MGSTSETKSPSEAAAEEBAFVFMQLTSASVLPVMTLSAIEDLVLEIMAKAGPGAHIS 60
DB 1 MGSTSETKSPSEAAAEEBAFVFMQLTSASVLPVMTLSAIEDLVLEIMAKAGPGAHIS 60
QY 61 TSDIASKLPTKNPDAVWMDRMLRLASYSVLTCSLRTPDGKIERLYGLAPVCKELTEN 120
DB 61 TSDIASKLPTKNPDAVWMDRMLRLASYSVLTCSLRTPDGKIERLYGLAPVCKELTEN 120
QY 121 DDGVSIAALSLNNQDQVLMESWYHLTEAVLEGGIPFNKAYGWTAFYHGTDPRFNTVFNN 180
DB 121 DDGVSIAALSLNNQDQVLMESWYHLTEAVLEGGIPFNKAYGWTAFYHGTDPRFNTVFNN 180
QY 181 GMSNHSITTMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIEE 240
DB 181 GMSNHSITTMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIEE 240
QY 241 AASYPEVEHVGGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCCYEALPTNGKYLAC 300
DB 241 AASYPEVEHVGGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCCYEALPTNGKYLAC 300
QY 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPGEGR-VALCAYNW 360
DB 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPGEGR-VALCAYNW 360
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AC Q43609;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DR 10-MAY-2005 (Rel. 47, Last annotation update)
DE Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-
DE methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOM
GN NameCOMT1;
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus;
OX NCBI_TaxID=3755;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=cv. Texas; TISSUE=Root;
RA Garcia-Mas J., Messeguer R., Arus P., Puigdomenech P.;
RT "The caffeic acid O-methyltransferase from Prunus amygdalus
RT (ex) Plant Gene Register PGR95-006.
RL FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
RL and of 5-hydroxyferulic acid to sinapic acid. The result
RL products may subsequently be converted to the correspond
RL alcohols that are incorporated into lignins.
CC -1 CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-
CC cinnamate.
CC -1 PATHWAY: Lignin biosynthesis.
CC -1 SIMILARITY: Belongs to the methyltransferase superfamily;
CC family. COMT subfamily.
CC -----
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CC use as long as its content is in no way modified and this statement
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CC -----
DR EMBL; X83217; CAA58218.1; -, mRNA.
DR HSSP; P28002; 1KYZ.
DR SMR; Q43609; 5-364.
DR InterPro; IPR012967; Dimerisation.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O Met trans2.
DR InterPro; IPR000051; SAM bind.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF08100; Dimerisation; 1.
DR Pfam; PF00891; Methyltransferase; 2; 1.
DR Lignin biosynthesis; Methyltransferase; Transferase.
KW SEQUENCE 365 AA; 39762 MW; C8C4BFE7E0180E7 CRC64;
SQ
Query Match 83.7%; Score 1602.5; DB 1; Length 365;
Best Local Similarity 82.8%; Pred. No. 2.5e-118;
Matches 304; Conservative 31; Mismatches 29; Indels 1;
QY 1 MGSTSETKSPSEAAAEEBAFVFMQLTSASVLPVMTLSAIEDLVLEIMAKAGPGAHIS 60
DB 1 MGSTSETKSPSEAAAEEBAFVFMQLTSASVLPVMTLSAIEDLVLEIMAKAGPGAHIS 60
QY 61 TSDIASKLPTKNPDAVWMDRMLRLASYSVLTCSLRTPDGKIERLYGLAPVCKELTEN 120
DB 61 TSDIASKLPTKNPDAVWMDRMLRLASYSVLTCSLRTPDGKIERLYGLAPVCKELTEN 120
QY 121 DDGVSIAALSLNNQDQVLMESWYHLTEAVLEGGIPFNKAYGWTAFYHGTDPRFNTVFNN 180
DB 121 DDGVSIAALSLNNQDQVLMESWYHLTEAVLEGGIPFNKAYGWTAFYHGTDPRFNTVFNN 180
QY 181 GMSNHSITTMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIEE 240
DB 181 GMSNHSITTMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIEE 240
QY 241 AASYPEVEHVGGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCCYEALPTNGKYLAC 300
DB 241 AASYPEVEHVGGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCCYEALPTNGKYLAC 300
QY 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPGEGR-VALCAYNW 360
DB 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPGEGR-VALCAYNW 360
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Db      299 ILVPADSLATKGVVHIDVIMLANNPGKERTDEBFQALAGAGQGFNVACS-AFNTY 357
Qy      361 IIEFLKK 367
Db      358 VIEFLKK 364

RESULT 3
COMT1 ROSCH STANDARD; PRT; 365 AA.
AC      08GU25;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-
GN      methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
OS      Rosa chinensis (China rose).
OC      Burkariya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC      rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
OX      NCBI_TaxId=74649;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=cv. Old Blush;
RA      Cock J.M., Scalliet G., Huguency P.;
RT      "Characterisation of a novel O-methyltransferase involved in the
RT      biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two
RT      major scent components of rose flowers.";
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
CC      and of 5-hydroxyferulic acid to sinapic acid. The resulting
CC      products may subsequently be converted to the corresponding
CC      alcohols that are incorporated into lignins.
CC      -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
CC      cinamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
CC      cinamate.
CC      -1- PATHWAY: Lignin biosynthesis.
CC      -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2
CC      family. COMT subfamily.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AJ439740; CAD29457.1; -; mRNA.
DR      HSSP; P28002; 1K1Z.
DR      SMR; Q8GU25; 5-365.
DR      InterPro; IPR012967; Dimerisation.
DR      InterPro; IPR001601; Methyltransf.
DR      InterPro; IPR001077; O Met. trans2.
DR      InterPro; IPR000051; SAM_bd.
DR      InterPro; IPR011991; Wing hlx DNA_bd.
DR      Pfam; PF08100; Dimerisation.1.
DR      Pfam; PF00891; Methyltransf.2; 1.
DR      KEGG; Lignin biosynthesis; Methyltransferase; Transferase.
SQ      SEQUENCE 365 AA; 39727 MW; C3E452559B64358 CRC64;

Query Match 83.6%; Score 1601.5; DB 1; Length 365;
Best Local Similarity 81.5%; Pred. No. 36-118;
Matches 300; Conservative 38; Mismatches 27; Indels 3; Gaps 2;

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Qy      121 DGVSIATSLMNOKVTLMESTYHLTEAVLEGIPPNKAYGNTATREYGT
Db      119 EDGVSIATSLMNOKVTLMESTYHLTEAVLEGIPPNKAYGNTATREYGT
Qy      181 GMSNSTITMKKILETYGFBGLGSDVVDGGGTGAHLMNIKAYPMIKI
Db      179 GNADSTITMKKILETYGFBGLTSDVVDGGGTGAHLMNIKAYPMIKI
Qy      241 APSYGEVHVGDMFVSVPKGDALFMKNI CHDMSDEHCLKFLKCYBALF
Db      239 AQYPGGVHVGDMFVSVPKGDALFMKNI CHDMSDEHCLKFLKCYBALF
Qy      301 ILVPADSLATKGVVHIDVIMLANNPGKERTDEBFQALAGAGQGFNR
Db      299 ILVPADSLATKGVVHIDVIMLANNPGKERTDEBFQALAGAGQGFNR
Qy      361 IIEFLKKI 368
Db      358 VIEFLKKI 365

RESULT 4
COMT1 POPTM STANDARD; PRT; 365 AA.
AC      000763; Q43094;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosyl-
GN      methionine:caffeic acid 3-O-methyltransferase 1) (COMT-1) (
OS      Populus tremuloides (Quaking aspen).
OC      Burkariya; Viridiplantae; Streptophyta; Embryophyta; Trache
OC      spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
OC      rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Pop
OX      NCBI_TaxId=3693;
RN      [1]
RP      NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 165-184; 335-3
RP      349-359.
RC      TISSUE=xylem;
RA      MEDLINE=92032785; PubMed=1932694;
RT      "Nucleotide sequence of a Populus tremuloides gene encoding
RT      caffeic acid/5-hydroxyferulic acid O-methyltransferase.";
RL      Plant Physiol. 107:1459-1459(1995).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RA      MEDLINE=9528573; PubMed=7770534; DOI=10.1104/pp.107.4.1459
RT      Tsai C.-J., Podila G.K., Chiang V.L.C.;
RT      "Nucleotide sequence of a Populus tremuloides gene encoding
RT      caffeic acid/5-hydroxyferulic acid O-methyltransferase.";
RL      Plant Physiol. 107:1459-1459(1995).
RN      [3]
RP      SEQUENCE REVISION.
RA      Tsai C.-J., Mielke M.R., Podila G.K., Chiang V.L.C.;
RL      Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      PROTEIN SEQUENCE OF 165-184; 335-346 AND 349-359.
RC      TISSUE=xylem;
RA      MEDLINE=92344802; PubMed=1368360; DOI=10.1016/0031-9422(92)
RT      Bugos R.C., Chiang V.L., Campbell W.H.;
RT      "Characterization of a Populus tremuloides caffeic acid/5-hydroxyferul
RT      methyltransferase from aspen.";
RL      Phytochemistry 31:1495-1498(1992).
CC      -1- FUNCTION: Catalyzes the conversion of caffeic acid to f
CC      and of 5-hydroxyferulic acid to sinapic acid. The result
CC      products may subsequently be converted to the correspon
CC      alcohols that are incorporated into lignins.
CC      -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihyd
CC      cinamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hyd
CC      cinamate.
CC      -1- PATHWAY: Lignin biosynthesis.

```

CC -1- TISSUE SPECIFICITY: Xylem.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2
CC family. COYT subfamily.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X62096; CAA44006.1; -; mRNA.
CC EMBL; U13171; AAB61731.1; -; Genomic DNA.
CC PIR; S18568; S18568.
CC HSSP; P28002; 1KXZ.
CC SMR; Q00763; 5-364.
CC InterPro; IPR012967; Dimerization.
CC InterPro; IPR001601; Methyltransf.
CC InterPro; IPR001077; O Met trans2.
CC InterPro; IPR000051; SAM bd.
CC InterPro; IPR011991; Wing_hlx_DNA_bd.
CC Pfam; PF08100; Dimerization_1.
CC Pfam; PF00891; Methyltransf_2; 1.
CC Direct protein sequencing; Lignin biosynthesis; Methyltransferase;
CC Transferrase.
SQ SEQUENCE 365 AA; 39805 MW; A6CECDBA4E0007CD CRC64;

Query Match 83.3%; Score 1595.5; DB 1; Length 365;
Best Local Similarity 80.9%; Pred. No. 8.9e-118;
Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;
QY 1 MGSSTETKSPSEAAAEAEAFVPMQLTSAVLPVMTLSAIELDVLEITMAKAGPAGHTS 60
DB 1 MGSSTETQMTPTQ--VSDEBAHIFAMQLASASVLPVMTLSAIELDVLEITMAKAGPAGHTS 58
QY 61 TSDIASKLPTKQPDAAVMDRLRLRLASYSVLTCSLRTLPDGKIERLYGLAPVCKFLTN 120
DB 59 TSEIASHLPTKQPDAAVMDRLRLRLASYSILTCSLKDLPDGKVERLYGLAPVCKFLTN 118
QY 121 DDGVSIALSLNQDKVLMESWYHLTEAVLEGGIPFNKAYGWTAPRYHGTDRFNTVFN 180
DB 119 EDGVSIALSLNQDKVLMESWYHLTEAVLEGGIPFNKAYGWTAPRYHGTDRFNTVFN 178
QY 181 GMSNSTITMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIBE 240
DB 179 GMSNSTITMKKILETYGFEGLGSVVDVGGGTGAHVNTIVSKYPIKGINFDLPVIBE 238
QY 241 APSYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCYEALPTNGKXVILAEC 300
DB 239 APSYGVHVGDMFVSPKGDALFMKWI CHDMSDAHCLKFLKNCYDALPENGKXVILVBC 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGRKERTKFEFLAKGAGREGRRVVASCAVNTW 360
DB 299 ILPVAPDTSLATKGVVHIDVIMLAHNPGRKERTKFEFLAKGAGREGRRVVASCAVNTW 357
QY 361 IIEFLKK 367
DB 358 VIEFLKK 364

OX NCBI_TaxID=197613;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE-Rose flower petals;
RC Wu S., Watanabe N., Mita S., Ueda Y., Shibuya M., Ebizuka Y
RT "Two O-methyltransferases isolated from flower petals of *Roi*
RT *chinnensis* var. *spontanea* involved in scent biosynthesis.";
RT J. Biosci. Bioeng. 0:0-0 (2003).
DR EMBL; AB086104; BAC78827.1; -; mRNA.
DR HSSP; P93324; 1EP1.
DR SMR; Q7X900; 5-365.
DR GO; GO:0008171; F:O-methyltransferase activity; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltran;
DR GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009809; P:Lignin biosynthesis; IEA.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O Met_trans2.
DR InterPro; IPR000051; SAM bind.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00891; Methyltransf_2; 1.
KW Methyltransferase; Transferrase.
SQ SEQUENCE 365 AA; 39669 MW; 2E46D4B039B65A70 CRC64;

Query Match 83.3%; Score 1595.5; DB 2; Length 36
Best Local Similarity 81.5%; Pred. No. 8.9e-118;
Matches 300; Conservative 37; Mismatches 28; Indels
QY 1 MGSSTETKSPSEAAAEAEAFVPMQLTSAVLPVMTLSAIELDVLEITM 60
DB 1 MGSSTETQMTPTQ--VSDEBAHIFAMQLASASVLPVMTLSAIELDVLEITM 58
QY 61 TSDIASKLPTKQPDAAVMDRLRLRLASYSVLTCSLRTLPDGKIERLYGL 120
DB 59 PNDLASQLPTKQPDAAVMDRLRLRLASYSILTCSLRTLPDGKVERLYGL 118
QY 121 DDGVSIALSLNQDKVLMESWYHLTEAVLEGGIPFNKAYGWTAPRYHGT 180
DB 119 EDGVSIALSLNQDKVLMESWYHLTEAVLEGGIPFNKAYGWTAPRYHGT 178
QY 181 GMSNSTITMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPMIGCI 240
DB 179 GMSNSTITMKKILETYGFEGLGSVVDVGGGTGAHVNTIVSKYPSIGCI 238
QY 241 APSYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCYEALP 300
DB 239 APQYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKNCYALP 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGRKERTKFEFLAKGAGREGRR 360
DB 299 ILPVAPDTSLATKGVVHIDVIMLAHNPGRKERTKFEFLAKGAGREGRR 357
QY 361 IIEFLKKI 368
DB 358 VIEFLKKI 365

RESULT 6
Q9M602_PRAAN PRELIMINARY; PRT; 365 AA.
ID Q9M602;
AC Q9M602;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE O-methyltransferase.
GN Name=omtl;
OS Fragaria ananassa (Strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots
OC euroids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=3747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kaldenhoff R., Wein M., Schwab W.;

Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB220491, AA28353.1; -, mRNA.
 DR HSSP: P28002, 1KYZ.
 DR SMR: Q9M602, 5-365.
 DR GO: GO:0008171, P:O-methyltransferase activity; IEA.
 DR GO: GO:0008175, P:S-adenosylmethionine-dependent methyltransferase; IEA.
 DR GO: GO:0016740, P:transferase activity; IEA.
 DR InterPro: IPR001601, Methyltransferase.
 DR InterPro: IPR001077, O-Mec_transf.
 DR InterPro: IPR000051, SAM_bind.
 DR InterPro: IPR011991, Wing_hlx_DNA_bd.
 DR Pfam: PF00891, Methyltransferase_2; 1.
 DR Methyltransferase; Transferase.
 DR KX SEQUENCE 365 AA; 39817 MW; EF748F753B55B0CB CRC64;
 SQ
 Query Match 83.0%; Score 1589.5; DB 2; Length 365;
 Best Local Similarity 81.0%; Pred. No. 2,7e-117;
 Matches 298; Conservative 39; Mismatches 28; Indels 3; Gaps 2;
 QY 1 MESTSETKMSPEBAABEAFVPMQLTSAVLPVMTKSAIELDVLEIMAKAGPGAHIS 60
 DB 1 MESTGETQMTPTQ--VSDEEAMLFAMQLASASVLPVMTKSAIELDVLEIMAKAGPGSFLS 58
 QY 61 TSDIASKLPTKAPDAVMDRLRLASYSVLTCSLRTLPDGKIBRLVGLAPVCKFLTEN 120
 DB 59 PBDLSAQLTAKPEAPVMDRLRLASYSILTCSLRTLPDGKIBRLVGLAPVCKFLTEN 118
 QY 121 DDGVSIALSLNODKVLMSWYHLTEAVLEGIPFNKA YGNTAFRHYGTDPRFNTVFN 180
 DB 119 EDGVSIALCLNODKVLMSWYHLKDVAIDGIPFNKA YGNTAFRHYGTDPRFNTVFN 178
 QY 181 GMSNSTITMKKILETTYKFGEGISVVDYGGGTGAHLNMIITAKYPMIKINFDLPVIEE 240
 DB 179 GMAHSHITMKKILETTYKFGEGIKSVVDYGGGTGAHVNMIVSKYPSIKGINFDLPVIED 238
 QY 241 APSYGEHVGDGMFVSYPKGDALFMKWI CHDMSDEHCKFLKCCYEAALPTNGKYLIAEC 300
 DB 239 APQYGEHVGDGMFVSYPKGNALFMKWI CHDMSDEHCKFLKCCYEAALPDGKYLIAEC 298
 QY 301 ILVPAADSLPTKAVVHIDVIMLANPGKERTKEFEALAKAGFEGFRVVASCAVNTW 360
 DB 299 ILVPAADSLPTKAVVHIDVIMLANPGKERTKEFEALAKAGSGRQGRVCCD-AFNTY 357
 QY 361 IIEFLKKI 368
 DB 358 VIEFLKKI 365
 RESULT 7
 COMTI_POPKI STANDARD; PRT; 365 AA.
 AC Q43046;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase 1) (COMT-1) (CAOMT-1). Name=HOMT1;
 GN Populus kitalakmensis (Aspen).
 OS Populus kitalakmensis (Aspen).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids 1; Malpighiales; Salicaceae; Salicaceae; Populus.
 OC NCBI_TaxId=3698;
 OK NCBI_TaxId=3698;
 RN NUCLEOTIDE SEQUENCE.
 RP Hayakawa T., Nanno K., Kawai S., Katayama Y., Moriohshi N.;
 RT "Molecular cloning and tissue-specific expression of two genes that encode caffeic acid O-methyltransferases from Populus kitalakmensis.", Plant Sci. 113:157-165 (1996).
 RL FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignine.

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydrocinamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydrocinamate.
 CC -1- PATHWAY: Lignin biosynthesis.
 CC -1- SIMILARITY: Belongs to the methyltransferase superfamily family. COMT subfamily.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EM
 CC the European Bioinformatics Institute. There are no restric
 CC use as long as its content is in no way modified and this s
 CC removed.
 CC -----
 CC DR EMBL: D49710, BAA08558.1; -, Genomic_DNA.
 DR HSSP: P28002, 1KYZ.
 DR SMR: Q43046, 5-364.
 DR InterPro: IPR012967, Dimerization.
 DR InterPro: IPR001601, Methyltransferase.
 DR InterPro: IPR001077, O-Mec_transf.
 DR InterPro: IPR000051, SAM_bd.
 DR InterPro: IPR011991, Wing_hlx_DNA_bd.
 DR Pfam: PF00891, Methyltransferase_2; 1.
 DR Pfam: PF00891, Methyltransferase_2; 1.
 DR Lignin biosynthesis; Methyltransferase; Transferase.
 DR KX SEQUENCE 365 AA; 39791 MW; D6005B10F55B83C CRC64;
 SQ
 Query Match 83.0%; Score 1588.5; DB 1; Length 3
 Best Local Similarity 80.7%; Pred. No. 3.2e-117;
 Matches 296; Conservative 36; Mismatches 32; Indels
 QY 1 MESTSETKMSPEBAABEAFVPMQLTSAVLPVMTKSAIELDVLEIM 15 60
 DB 1 MESTGETQMTPTQ--VSDEEAMLFAMQLASASVLPVMTKSAIELDVLEIM 15 58
 QY 61 TSDIASKLPTKAPDAVMDRLRLASYSVLTCSLRTLPDGKIBRLVGL 15 120
 DB 59 TSEIASHLPTKAPDAVMDRLRLASYSILTCSLRTLPDGKIBRLVGL 15 118
 QY 121 DDGVSIALSLNODKVLMSWYHLTEAVLEGIPFNKA YGNTAFRHYG 15 180
 DB 119 EDGVSIVPLCLNODKVLMSWYHLKDVAIDGIPFNKA YGNTAFRHYG 15 178
 QY 181 GMSNSTITMKKILETTYKFGEGISVVDYGGGTGAHLNMIITAKYPMIKI 15 240
 DB 179 GMSHSHITMKKILETTYKFGEGITSLVDYGGGTGAHVNTIYKPSIKGI 15 238
 QY 241 APSYGEHVGDGMFVSYPKGDALFMKWI CHDMSDEHCKFLKCCYEA 15 300
 DB 239 APSYGEHVGDGMFVSYPNADAVFMKWI CHDMSAHCKFLKCCYDALP 15 298
 QY 301 ILVPAADSLPTKAVVHIDVIMLANPGKERTKEFEALAKAGFEGFR 15 360
 DB 299 ILVPAADSLPTKAVVHIDVIMLANPGKERTKEFEALAKAGAFQGRE 15 357
 QY 361 IIEFLKK 367
 DB 358 VIEFLKK 364
 RESULT 8
 ID Q9M569, PROTI PRELIMINARY; PRT; 360 AA.
 AC Q9M569;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Caffeic acid O-3-methyltransferase (Fragment).
 GN Name=COMT;
 OS Populus tomentosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eustosids 1; Malpighiales; Salicaceae; Salicaceae; Populus.
 OC NCBI_TaxId=118781;
 OK NCBI_TaxId=118781;

RT "Stress responses in alfalfa (*Medicago sativa* L.). X. Molecular cloning
 RT and expression of S-adenosyl-L-methionine:caffeic acid 3-O-
 methyltransferase, a key enzyme of lignin biosynthesis.";
 RL Plant Physiol. 97:7-14(1991).
 CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
 CC and of 5-hydroxyferulic acid to sinapic acid. The resulting
 CC products may subsequently be converted to the corresponding
 CC alcohols that are incorporated into lignins.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
 CC cinnamate -> S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
 CC cinnamate.
 CC -1- PATHWAY: Lignin biosynthesis.
 CC -1- TISSUE SPECIFICITY: More abundant in roots and stems.
 CC -1- INDUCTION: By infection, plant wounding, or elicitor treatment of
 CC cell cultures.
 CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2
 CC family. COMT subfamily.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: M63853; AAB46623.1; -, mRNA.
 DR PIR: T09673; T09673.
 DR PDB: 1KRW; X-ray; A/C/F=a1-365.
 DR PDB: 1KYZ; X-ray; A/C/E=a1-365.
 DR InterPro: IPR012967; Dimerisation.
 DR InterPro: IPR01601; Methyltransferase.
 DR InterPro: IPR001077; O Met trans2.
 DR InterPro: IPR000051; SAM_bd.
 DR InterPro: IPR011991; Wing_hlx_DNA_bd.
 DR Pfam: PF08100; Dimerisation; 1.
 DR Pfam: PF00891; Methyltransferase; 2; 1.
 KM 3D-structure; Lignin biosynthesis; Methyltransferase; Transferase.
 FT HELIX 16 27
 FT TURN 28 30
 FT HELIX 31 41
 FT TURN 42 43
 FT HELIX 44 49
 FT TURN 50 51
 FT TURN 53 54
 FT STRAND 57 57
 FT HELIX 59 64
 FT TURN 65 65
 FT TURN 71 72
 FT HELIX 73 86
 FT TURN 87 88
 FT STRAND 90 96
 FT TURN 98 99
 FT STRAND 102 108
 FT HELIX 110 115
 FT TURN 119 120
 FT TURN 124 124
 FT TURN 125 131
 FT HELIX 132 132
 FT TURN 133 137
 FT HELIX 138 142
 FT HELIX 143 149
 FT HELIX 153 158
 FT HELIX 162 165
 FT HELIX 166 168
 FT HELIX 170 194
 FT TURN 197 198
 FT STRAND 203 207
 FT TURN 208 208
 FT TURN 210 211
 FT HELIX 213 221
 FT TURN 223 224
 FT STRAND 226 231
 FT TURN 233 238
 FT TURN 243 244

FT STRAND 245 249
 FT TURN 252 254
 FT STRAND 262 263
 FT TURN 269 270
 FT HELIX 273 286
 FT STRAND 293 297
 FT STRAND 299 300
 FT STRAND 308 323
 FT STRAND 330 331
 FT STRAND 332 342
 FT HELIX 347 353
 FT TURN 354 355
 FT STRAND 356 361
 SQ SEQUENCE 365 AA; 39946 MW; C14B0D75F979C6B6 CRC64;
 Query Match 80.7%; Score 1544.5; DB 1; Length 3
 Best Local Similarity 78.8%; Pred. No. 9,7e-114;
 Matches 290; Conservative 42; Mismatches 33; Indels
 QY 1 MGSTETKMSPEEAAAEBAFVPMOUTSASVLPMTLSAIEDVLEIK IS 60
 DB 1 MGSTGETQITPTTH--ISDEBANLPMQLASASVLPMTILKSALELDLEII IS 58
 QY 61 TSDIASKLPTKQPDAAVMLDRMLRLASYSVLTGSLRTLPDGIKIRLYGL RN 120
 DB 59 PLEIASQLPTNPDPAPVMDRLRLACIYITGCVRTQDQDKVRLVGL KN 118
 QY 121 DDGVSIAALSINODKVLMSWYHLTEAVLEGIPFNKAYGWTAFEVHGT NN 180
 DB 119 EDGVSISALNLNNOQKVLMSWYHLKDAVLGDIQGFNNAYGWTAFEVHGT NK 178
 QY 181 GMSNHSITTKKILETYGFGFGLGSVDVGGTGTGHLMMIITAKYPMIGI EE 240
 DB 179 GMSDHSITTKKILETYGFGFGLKSLVDVGGGTGAVINTIYSKYPTIKGI ED 238
 QY 241 APSYGVHVGSDMVSVPKGDAPFMKMICDMSDEHCLKFLKCYEALP EC 300
 DB 239 APSYGVHVGSDMVSIPKADAVPMKMICDMSDEHCLKFLKCYEALP EC 298
 QY 301 ILPVPDASLPTRKAVVHIDVIMLANPGKERTKTEKFPALAKGAGFEGRR TW 360
 DB 299 ILPVPDSSLATKGVVHIDVIMLANPGKERTQKEFPDLAKGAGFQGRK TY 357
 QY 361 IIEFLKKI 368
 DB 358 IMEFLKKV 365
 RESULT 11
 COMTI_EUCGU
 ID COMTI_EUCGU STANDARD; PRT; 366 AA.
 AC P46484;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl
 DE methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOM
 GN Name=OMT;
 OS Eucalyptus gunnii (Cider tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
 OC rosidae; Myrtales; Myrtaceae; Eucalyptus.
 OC NCBI_TaxID=3933;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Xylem;
 RX MEDLINE=94345011; PubMed=8066135; DOI=10.1104/pp.105.2.749;
 RA Poeydomegne O.; Boudet A.M.; Grima-Pettenati U.;
 RT "A cDNA encoding S-adenosyl-L-methionine:caffeic acid 3-O-
 RL methyltransferase from Eucalyptus.";
 RL Plant Physiol. 105:749-750(1994).
 CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to f
 CC and of 5-hydroxyferulic acid to sinapic acid. The resul

DB 1 MGSQTGAETQTLPTN--VSDEANLPMQQLASAVLPMVLKKAILEDLVLEIMAKSIPIHGS 58
QY 56 GAHITSIDIASLPTKPNPDAAVMDRLMLLASISVLTCSLTLPDGKIERLYGALPYCK 115
DB 59 GAYISPAEIAQQLPTTNDAPVLMRLVRLRLASYSVWTCISLELDPGKERLYGLAPYCK 118
QY 116 FLTRDDGVSTIALSLMNODKYLMSWYHLTEAVLEGIPFNKAYGMTAFEHGTDPRPN 175
DB 119 FLTKNEDGVSLAPLCLMNODKYLMSWYHLKDALIDGGIPFNKAYGMTAFEHGTDPRPN 178
QY 176 TVFNNGMSNSTIITMKKILETYGFEGLGSVVDVGGTGGAHLNMIYAKYPMKGINFDLP 235
DB 179 KYFNNGMSDHSITITMKKIFEMVTGFEALNTITVDVGGTGGAVALSMIVAKYPSIKGINFDLP 238
QY 236 HYIEAPSPYGVHVGGMFVSVPKGDALFMKMICHDMSDEHCLKFLKCYALPTNGKV 295
DB 239 HYIEDAPTPYGVHVGGMFVSVPKGDALFMKMICHDMSDEHCLKFLKCYALTEHGV 298
QY 296 ILAECILPVPAPDASLPTKAVVHIDVIMLANPGKERTKEFEALAKGAFEPFVAVSC 355
DB 299 IVAECILPUSPSPSLATKGVHIDVIMLANPGKERTKEFEALALIGAFKGR-VACC 357
QY 356 AYNTHWIEFLK 366
DB 358 AFNTYVMEFLK 368

RESULT 13
COMT1 CAPAN STANDARD; PRT; 359 AA.
ID COMT1 CAPAN
AC 09RGY8; P93088;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
GN Name=COMT;
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxId=4072;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pericarp;
RA Lee B.-H., Choi D., Lee K.-W.;
RA "Isolation and characterization of o-diphenol-O-methyltransferase cDNA clone in hot pepper (Capsicum annuum L.).";
RL J. Plant Biol. 41:9-14(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Chungyang; TISSUE=Root;
RA Kim K.-W., Lee S.-W.;
RA "Isolation and characterization of caffeic acid O-methyltransferase cDNA from Capsicum annuum.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-cinnamate.
CC -1- PATHWAY: Lignin biosynthesis.
CC -1- TISSUE SPECIFICITY: Fruit. Not expressed in leaf.
CC -1- DEVELOPMENTAL STAGE: Expression increases during fruit development but decreases during ripening.
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2 family. COMT subfamily.
CC -----
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CC use as long as its content is in no way modified and this s
CC removed.
CC EMBL; U83789; AAC1745.1; -; mRNA.
CC EMBL; AF212316; AAG43822.1; -; mRNA.
CC HSSP; P28002; 1KYZ.
DR SMR; Q9FOY8; 11-359.
DR InterPro; IPR012967; Dimerisation.
DR InterPro; IPR001601; Methyltransferase.
DR InterPro; IPR001077; O-Met. trans2.
DR InterPro; IPR011991; Wing hlx DNA_bd.
DR Pfam; PF00891; Methyltransferase 1.
DR Pfam; PF08100; Dimerisation.
KM Lignin biosynthesis; Methyltransferase; Transferase.
FT CONFLICT 71 71 V -> I (in Ref. 2).
FT CONFLICT 246 246 R -> G (in Ref. 2).
SQ SEQUENCE 359 AA; 39433 MW; 70599AED75CE1730 CRC64;
Query Match 79.8%; Score 1527.5; DB 1; Length 3
Best Local Similarity 77.9%; Pred. No. 2.1e-112;
Matches 285; Conservative 35; Mismatches 39; Indels

QY 1 MGSSTETKMSPEEAAREBAFVPMQLTSSAVLPMVLSKAILEDVLEIM 1S 60
DB 1 MDSTNQ-----NLQTDEAFLPMQLASASVLPMLKSALEDLLEIM 1S 54
QY 61 TSDIASKLPTKNPDAAVMDRLMLLASISVLTCSLTLPDGKIERLYGL 1N 120
DB 55 PSEIAAQPTKNPEAPVMDRLRLATYSVLTCTLRTLPDGRVRLVSL 1N 114
QY 121 DDGVSTIALSLMNODKYLMSWYHLTEAVLEGIPFNKAYGMTAFEVGT 1N 180
DB 115 ADGVSAVPLLMNODKYLMSWYHLTDVLDGVGFENAYGMTAFEVGT 1N 174
QY 181 GMSNSTITMKKILETYGFEGLGSVVDVGGTGGAHLNMIYAKYPMKGI 1E 240
DB 175 GMSDHSITMKKILEDYGFEGLSIVDVGGTGATVAMYSKYSISGI 1E 234
QY 241 APSYGVHVGGMFVSVPKGDALFMKMICHDMSDEHCLKFLKCYEALP 1E 300
DB 235 APAYGVHVGGMFVSVPKADALFMKMICHDMSDEHCLKFLKCYEALP 1E 294
QY 301 ILPVPAPDASLPTKAVVHIDVIMLANPGKERTKEFEALAKGAFBEGR 1T 360
DB 295 ILPPTPDTSAATKXAVHIDVIMLANPGKERTKEFEALAKGAFETGR 1T 353
QY 361 IIEFLK 366
DB 354 VMEFHK 359

RESULT 14
COMT1 OCIBA STANDARD; PRT; 361 AA.
ID COMT1 OCIBA
AC 09XGW0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase 1) (COMT-1) (Name=COMT1);
GN Ocimum basilicum (Sweet basil).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Lamiales; Lamiales; Nepetoideae; Ocimeae
OX NCBI_TaxId=39350;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. EMK-1;
RA Wang J., Dudareva N., Kish C.M., Simon J.E., Lewinson E., Pichersky E.;
RA "Nucleotide sequences of two cDNAs encoding caffeic acid O-

Mon Dec 12 10:52:55 2005

us-10-681-878a-6.rup

ge 11

Db 357 VIEFRKQ 363

Search completed: December 12, 2005, 08:37:26
Job time : 234 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 08:30:15 , Search time 46 Seconds
(without alignments)
661.405 Million cell updates/sec

Title: US-10-681-878A-6

Perfect score: 1915

Sequence: 1 MGS1SETKMSPEAAAE...PRVASCANWTITFLKKI 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/1aa/6_COMB.pep:*

3: /cgn2_6/prodata/1/1aa/H_COMB.pep:*

4: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*

5: /cgn2_6/prodata/1/1aa/RG_COMB.pep:*

6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1915	100.0	368	2	US-08-991-677-6
2	1595.5	83.3	365	1	US-08-715-325-2
3	1595.5	83.3	365	2	US-09-947-027-6
4	1572.5	82.1	364	1	US-08-204-288-2
5	1566.5	81.8	365	2	US-09-500-569-4
6	1566.5	81.8	365	2	US-09-971-823B-4
7	1499.5	78.3	364	1	US-08-204-288-5
8	1492	77.9	358	2	US-09-500-569-18
9	1492	77.9	358	2	US-09-971-823B-18
10	1244	65.0	356	2	US-09-500-569-6
11	1244	65.0	356	2	US-09-971-823B-6
12	1073	56.0	362	2	US-09-500-569-14
13	1073	56.0	362	2	US-09-971-823B-14
14	1047	54.7	365	1	US-08-186-833-4
15	1045.5	54.6	365	1	US-08-204-288-7
16	988.5	51.6	354	2	US-09-500-569-12
17	988.5	51.6	354	2	US-09-971-823B-12
18	964.5	50.4	264	2	US-09-598-401C-78
19	947	49.5	305	2	US-09-500-569-2
20	947	49.5	305	2	US-09-971-823B-2
21	779.5	40.7	231	2	US-09-500-569-20
22	779.5	40.7	231	2	US-09-971-823B-20
23	771	40.3	378	2	US-09-500-569-10
24	771	40.3	378	2	US-09-971-823B-10
25	726	37.9	371	2	US-09-500-569-16
26	726	37.9	371	2	US-09-971-823B-16
27	667	34.8	328	2	US-09-615-192A-274

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29	500.5	26.1	174	2	US-09-971-823B-26	Seqn	Appl
30	479	25.0	198	2	US-09-615-192A-271	Seqn	Appl
31	413.5	21.6	156	2	US-09-615-192A-272	Seqn	Appl
32	376.5	19.7	160	2	US-09-615-192A-275	Seqn	Appl
33	372	19.4	188	2	US-09-500-569-8	Seqn	Appl
34	372	19.4	188	2	US-09-971-823B-8	Seqn	Appl
35	365	18.1	145	2	US-09-615-192A-270	Seqn	Appl
36	356.5	18.6	94	1	US-08-266-451B-20	Seqn	Appl
37	356.5	18.6	94	1	US-08-748-725-20	Seqn	Appl
38	291.5	15.2	313	2	US-09-902-540-9934	Seqn	Appl
39	272.5	14.2	363	1	US-08-845-742-2	Seqn	Appl
40	259	13.5	362	2	US-09-758-759-196	Seqn	Appl
41	254.5	13.3	332	2	US-09-724-797-18	Seqn	Appl
42	249.5	13.0	351	1	US-09-266-965-133	Seqn	Appl
43	226	11.8	82	2	US-09-500-569-24	Seqn	Appl
44	226	11.8	82	2	US-09-971-823B-24	Seqn	Appl
45	217.5	11.4	345	2	US-09-059-522-5	Seqn	Appl
46	217.5	11.4	345	2	US-09-382-027-5	Seqn	Appl
47	212.5	11.1	621	2	US-09-059-522-1	Seqn	Appl
48	212.5	11.1	621	2	US-09-382-027-1	Seqn	Appl
49	211.5	11.0	452	2	US-09-059-522-3	Seqn	Appl
50	211.5	11.0	452	2	US-09-382-027-3	Seqn	Appl
51	186.5	9.7	356	1	US-07-959-941-2	Seqn	Appl
52	186.5	9.7	356	1	US-08-259-924-2	Seqn	Appl
53	173	9.0	115	2	US-09-266-965-4	Seqn	Appl
54	171.5	9.0	123	2	US-09-500-569-28	Seqn	Appl
55	171.5	9.0	123	2	US-09-971-823B-28	Seqn	Appl
56	166.5	8.7	109	2	US-09-500-569-22	Seqn	Appl
57	166.5	8.7	109	2	US-09-971-823B-22	Seqn	Appl
58	147.5	7.7	117	2	US-09-266-965-5	Seqn	Appl
59	146	7.6	115	2	US-09-266-965-3	Seqn	Appl
60	141	7.4	125	2	US-09-902-540-10705	Seqn	Appl
61	112.5	5.9	368	2	US-09-252-991A-20452	Seqn	Appl
62	107	5.6	139	2	US-09-252-991A-20476	Seqn	Appl
63	100.5	5.2	308	1	US-08-457-245-8	Seqn	Appl
64	91.5	4.8	237	1	US-08-576-626A-58	Seqn	Appl
65	91	4.8	379	2	US-09-489-039A-12857	Seqn	Appl
66	91	4.8	573	2	US-09-134-000C-5258	Seqn	Appl
67	89.5	4.7	482	2	US-09-252-991A-17621	Seqn	Appl
68	89	4.6	578	2	US-09-489-039A-14097	Seqn	Appl
69	89	4.6	578	2	US-09-949-016-6961	Seqn	Appl
70	88.5	4.6	522	2	US-09-902-540-12872	Seqn	Appl
71	86.5	4.5	437	2	US-09-602-777A-84	Seqn	Appl
72	86	4.5	439	2	US-09-134-000C-6557	Seqn	Appl
73	86	4.5	483	2	US-08-378-313-31	Seqn	Appl
74	85.5	4.5	603	2	US-08-687-865A-2	Seqn	Appl
75	85.5	4.5	603	2	US-07-642-734C-5	Seqn	Appl
76	85.5	4.5	3170	2	US-08-439-009A-5	Seqn	Appl
77	84.5	4.4	911	1	US-08-596-985-2	Seqn	Appl
78	84.5	4.4	268	2	US-09-543-681A-7944	Seqn	Appl
79	84	4.4	290	2	US-09-543-681A-4737	Seqn	Appl
80	84	4.4	614	2	US-10-104-047-3276	Seqn	Appl
81	84	4.4	897	2	US-09-543-681A-4249	Seqn	Appl
82	84	4.4	510	2	US-08-801-344-8	Seqn	Appl
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84	83	4.3	510	2	US-09-115-475-19	Seqn	Appl
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86	82.5	4.3	671	1	US-08-737-716-13	Seqn	Appl
87	82	4.3	769	2	US-09-543-681A-7175	Seqn	Appl
88	82	4.3	803	2	US-08-246-982A-6	Seqn	Appl
89	82	4.3	803	2	US-08-062-368-4	Seqn	Appl
90	81.5	4.3	609	2	US-09-115-475-19	Seqn	Appl
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94	81.5	4.3	3144	1	US-08-453-265-6	Seqn	Appl
95	81.5	4.3	3144	1	US-08-453-273B-42	Seqn	Appl
96	81.5	4.3	3144	1	US-08-556-419-21	Seqn	Appl
97	81.5	4.3	3144	2	US-09-041-886-15	Seqn	Appl
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99	81	4.2	245	2	US-09-724-797-14	Seqn	Appl
100	81	4.2	313	2	US-09-134-001C-3628	Seqn	Appl

ALIGNMENTS

RESULT 1
US-08-991-677-6
; Sequence 6, Application US/08991677A
; Patent No. 6252135
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Carriaway, Daniel T
; APPLICANT: Smeltzer, Richard H
; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
; FILE REFERENCE: 50617
; CURRENT APPLICATION NUMBER: US/08/991,677A
; FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: US 60/033,381
; EARLIER FILING DATE: 1996-12-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Liquidambar styraciflua
US-08-991-677-6

Query Match 100.0%; Score 1915; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGSTSETKMSPSBAABEBAFVFMQLTSASVLPVMTLSAIELDVLEIMAKAGPGAHIS 60

QY 61 TSDIASKLPKTPKPDAAVMDRLRLRLASYSVLTCSLRTLPDGKIERLYGLAPVCKFLTEN 120
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DB 61 TSDIASKLPKTPKPDAAVMDRLRLRLASYSVLTCSLRTLPDGKIERLYGLAPVCKFLTEN 120

QY 121 DDGVSIALSLMNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFYHGTDRFNTVFNN 180
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DB 121 DDGVSIALSLMNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFYHGTDRFNTVFNN 180

QY 181 GMSNHSITTMKILLETYYKGFEGSLGVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIVE 240
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DB 181 GMSNHSITTMKILLETYYKGFEGSLGVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIVE 240

QY 241 APSYGVHEHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYEALPTNGKVI LAEC 300
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DB 241 APSYGVHEHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYEALPTNGKVI LAEC 300

QY 301 ILPVPADASLPTKAVVHIDVIMLAHNPCKERTKTEKFEALAGAGEGRRVVASCAVNTW 360
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DB 301 ILPVPADASLPTKAVVHIDVIMLAHNPCKERTKTEKFEALAGAGEGRRVVASCAVNTW 360

QY 361 IIEFLKKI 368
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DB 361 IIEFLKKI 368
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RESULT 2
US-08-715-325-2
; Sequence 2, Application US/08715325
; Patent No. 5886243
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Teal, Chung-Tui
; APPLICANT: Podila, Gopi
; TITLE OF INVENTION: Genetic Engineering of Wood Color
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
ADDRESSES: Michael, Best & Friedrich

STREET: 100 E. Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: United States of America
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: WordPerfect for Windows 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,325
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US60/007727
FILING DATE: 30 NOV 1995
ATTORNEY/AGENT INFORMATION:
NAME: Gemignani, Joseph A
REGISTRATION NUMBER: 19,482
REFERENCE/DOCKET NUMBER: 66040/9627
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 271-6560
TELEFAX: (414) 277-0656
TELEX: 262057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHEICAL: no
US-08-715-325-2

Query Match 83.3%; Score 1595.5; DB 1; Length 365
Best Local Similarity 80.9%; Pred. No. 7.8e-169;
Matches 297; Conservative 37; Mismatches 30; Indels 2;

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DB 1 MGSTSETQMTPTQ--VSDBEHLTFAMQLASASVLPMLIKTALIEDLLEIM 58

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DB 59 TSELSHLPKTPKPDAPVMDRLRLRLASYSVLTCSLRTLPDGKIERLYGL 118

QY 121 DDGVSIALSLMNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFYHGT 180
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DB 119 DDGVSIVPLCLMNQDKVLMESWYHLTKDAI LDGGRIPFNKAYGWTAFYHGT 178

QY 181 GMSNHSITTMKILLETYYKGFEGSLGVVDVGGGTGAHLNMIIAKYPMI 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 179 GMSDHSITTMKILLETYYKGFEGSLGVVDVGGGTGAHLNMIIAKYPMI 238

QY 241 APSYGVHEHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYEALP 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 239 APSYGVHEHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYEALP 298

QY 301 ILPVPADASLPTKAVVHIDVIMLAHNPCKERTKTEKFEALAGAGEGRR 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 361 IIEFLKK 367
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 358 VIEFRKK 364
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RESULT 3
US-09-947-027-6
; Sequence 6, Application US/09947027
; Patent No. 685864
; GENERAL INFORMATION:

APPLICANT: Chiang, Vincent Lee C.
APPLICANT: Li, Laigeng
TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITIO
TITLE OF INVENTION: CELLULOSE CONTROL IN PLANTS
FILE REFERENCE: 066040-9718
CURRENT APPLICATION NUMBER: US/09/947,027
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: 60/230,086
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 6
LENGTH: 365
TYPE: prt
ORGANISM: aegon populus tremuloides
US-09-947-027-6

Query Match 83.3%; Score 1595.5; DB 2; Length 365;
Best Local Similarity 80.9%; Pred. No. 7.8e-169;
Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;

QY 1 MGSTSETKMSPEBAABEBAFVPMOLTSASVLPMTLSAIELDVLEIMAKAGAHIS 60
1 MGSTSETQMTPTQ--VSDEBAHLFANQLASASVLPMTLTAIELDLLEIMAKAGAHIS 58
DB 61 TSDIASKLPTRKPDAAVMDRLRLASVYVTCSLRTLPDGIKIERLYGLAPVCKFLRN 120
59 TSEIASHLPTRKPDAPVMDRLRLRLASYSILTCSLKDPDKKVERLYGLAPVCKFLRN 118
QY 121 DGVGSIALLSLMNODKVLMSWYHLTEAVLBGGIPFNKAYGNTAFPHGTDRPMTVFN 180
119 EDGVSVPCLMNODKVLMSWYHLKDAIILDGIPFNKAYGNTAFPHGTDRPMTVFN 178
QY 181 GMSNSTITMKKILETYKGFEGISVVDVGGGTGAHLNMIKAYPMIKINFDPLEHVE 240
179 GMSDSTITMKKILETYKGFEGISLVVDVGGGTGAHVNTIVSKYPSIKINFDPLEHVE 238
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239 APSYGEVHVGDMPVSVKADAVPMKMICHDMSDAHCLFKKCYDALPENGKYLAE 298
DB 301 ILPVAPDASLPTKAVVHIDVIMLANPGKERTKEFEALAKAGPFGPRVAVCAVNTW 360
299 ILPVAPDTSLATKGVVHIDVIMLANPGKERTKEFEALAKAGPFGPRVAVCAVNTW 357
QY 361 IIEFLK 367
DB 358 VIEFLK 364

RESULT 4
US-08-204-288-2
Sequence 2, Application US/08204288
Patent No. 5959178
GENERAL INFORMATION:
APPLICANT: VAN DOORSELAERE, Jan
APPLICANT: FRITIG, Bernard J.M.
APPLICANT: INZE, Dirk G.
APPLICANT: JOUANIN, Lise
APPLICANT: KNIGHT, Mary E.
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LERAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3518
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-288-2

Query Match 82.1%; Score 1572.5; DB 1; Length 3
Best Local Similarity 80.3%; Pred. No. 2.8e-166;
Matches 294; Conservative 36; Mismatches 33; Indels 2;

QY 1 MGSTSETKMSPEBAABEBAFVPMOLTSASVLPMTLSAIELDVLEIM 60
1 MGSTSETQMTPTQ--VSDEBAHLFANQLASASVLPMTLTAIELDLLEIM 58
DB 61 TSDIASKLPTRKPDAAVMDRLRLASVYVTCSLRTLPDGIKIERLYGL 120
59 TSEIASHLPTRKPDAPVMDRLRLRLASYSILTCSLKDPDKKVERLYGL 118
QY 121 DGVGSIALLSLMNODKVLMSWYHLTEAVLBGGIPFNKAYGNTAFPHGT 180
119 EDGVSVPCLMNODKVLMSWYHLKDAIILDGIPFNKAYGNTAFPHGT 178
QY 181 GMSNSTITMKKILETYKGFEGISVVDVGGGTGAHLNMIKAYPMIKI 240
179 GMSDSTITMKKILETYKGFEGISLVVDVGGGTGAHVNTIVSKYPSIKI 238
QY 241 APSYGEVHVGDMPVSVKGDALFMKMICHDMSDEHCLFKKCYEALP 300
239 APSYGEVHVGDMPVSVKADAVPMKMICHDMSDAHCLFKKCYDALP 298
DB 301 ILPVAPDASLPTKAVVHIDVIMLANPGKERTKEFEALAKAGPFGPR 360
299 ILPVAPDTSLATKGVVHIDVIMLANPGKERTKEFEALAKAGPFGPR 357
QY 361 IIEFLK 366
DB 358 VIEFLK 363

RESULT 5
US-09-500-569-4
Sequence 4, Application US/09500569
Patent No. 6329204
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jemie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase

```
/ FILE REFERENCE: B81327 US NA
/ CURRENT APPLICATION NUMBER: US/09/500,569
/ CURRENT FILING DATE: 2000-02-09
/ EARLIER APPLICATION NUMBER: 60/119,587
/ EARLIER FILING DATE: 1999-February-10
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 4
/ LENGTH: 365
/ TYPE: PRT
/ ORGANISM: Glycine max
US-09-500-569-4

Query Match      81.8%; Score 1566.5; DB 2; Length 365;
Best Local Similarity 80.2%; Pred. No. 1.3e-165;
Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGSSTSTKSPSEAAAEAEAFVAMQLTASAVLPVNLKSAIEDLVLEIMAKAGPGAHIS 60
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MGSSTGTQITPTH--VSDEBANLFAMQLASASVLPMLILKSALELDLEIIAKAGPGVHLS 58

QY 61 TSDIASKLPTKPNDAVMDRLMLLASVLTGSLRTLPDGKIERLYGGLAPYCKRLTN 120
   :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 59 PTDISSQLPTQNPDAFVMDRLIRLLACYNILSFSRLTPDGKVERLYGLAPVAKYLVKN 118

QY 121 DDGVSIAALSLMNQDKVLMESWYHLTEAVLLEGGIPFNKAYGNTAFYHGTDPRENTVFN 180
   :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 119 EDGVSIAALMNQDKVLMESWYHLKDAVLLEGGIPFNKAYGNTAFYHGTDRENFVFNK 178

QY 181 GMSNHTTMMKILLETYGFGFGLGSVDVGGGTGAHLNMIIAKYPMIKGINFDPHVEE 240
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 179 GMADHSTITMKILLETYGFESLSKSLVDVGGGTGAVINMIVSKHPTIKGINFDPHVID 238

QY 241 APSYGEHVGGDMFVSVPKGDALFMKWI CHDMSDEHCKLFKCYEALPTGKXYLAAC 300
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 239 APSYGEHVGGDMFASVPKADALFMKWI CHDMSDEHCKLFKNCYCALPDNGKXYVAEC 298

QY 301 ILPVAPDASLPTKAVVHIDVIMLANHPGKERTKEFEALAKAGFEGFRVVAACAYNTW 360
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 299 ILPVAPDSSLATKGVVHIDVIMLANHPRKERTKEFEALAKGSGFGFRVVC-CAFNIN 357

QY 361 IIEFLKKI 368
   |||:::|
Db 358 IMEFLKKI 365

RESULT 6
US-09-971-823B-4
/ Sequence 4, Application US/0971823B
/ Patent No. 6610521
/ GENERAL INFORMATION:
/ APPLICANT: Cahoon, Rebecca E.
/ TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
/ FILE REFERENCE: B81327 US NA
/ CURRENT APPLICATION NUMBER: US/09/971,823B
/ CURRENT FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 60/119,587
/ PRIOR FILING DATE: 1999-02-10
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 4
/ LENGTH: 365
/ TYPE: PRT
/ ORGANISM: Glycine max
US-09-971-823B-4

Query Match      81.8%; Score 1566.5; DB 2; Length 365;
Best Local Similarity 80.2%; Pred. No. 1.3e-165;
Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGSSTSTKSPSEAAAEAEAFVAMQLTASAVLPVNLKSAIEDLVLEIMAKAGPGAHIS 60
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MGSSTGTQITPTH--VSDEBANLFAMQLASASVLPMLILKSALELDLEIIAKAGPGVHLS 58
```

```
QY 61 TSDIASKLPTKPNDAVMDRLMLLASVLTGSLRTLPDGKIERLYGL 120
   :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 59 PTDISSQLPTQNPDAFVMDRLIRLLACYNILSFSRLTPDGKVERLYGL 118

QY 121 DDGVSIAALSLMNQDKVLMESWYHLTEAVLLEGGIPFNKAYGNTAFYHGTD 180
   :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 119 EDGVSIAALMNQDKVLMESWYHLKDAVLLEGGIPFNKAYGNTAFYHGTD 178

QY 181 GMSNHTTMMKILLETYGFGFGLGSVDVGGGTGAHLNMIIAKYPMIKGIN 240
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 179 GMADHSTITMKILLETYGFESLSKSLVDVGGGTGAVINMIVSKHPTIKGIN 238

QY 241 APSYGEHVGGDMFVSVPKGDALFMKWI CHDMSDEHCKLFKCYEALP 300
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 239 APSYGEHVGGDMFASVPKADALFMKWI CHDMSDEHCKLFKNCYCALP 298

QY 301 ILPVAPDASLPTKAVVHIDVIMLANHPGKERTKEFEALAKAGFEGFR 360
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 299 ILPVAPDSSLATKGVVHIDVIMLANHPRKERTKEFEALAKGSGFGFR 357

QY 361 IIEFLKKI 368
   |||:::|
Db 358 IMEFLKKI 365

RESULT 7
US-08-204-288-5
/ Sequence 5, Application US/08204288
/ Patent No. 5959178
/ GENERAL INFORMATION:
/ APPLICANT: VAN DOORSELAERE, Jan
/ APPLICANT: FRITIG, Bernhard J.M.
/ APPLICANT: INZE, Dirk G.
/ APPLICANT: JOUANIN, Lise
/ APPLICANT: KNIGHT, Mary E.
/ APPLICANT: LEGRAND, Michel
/ TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
/ TITLE OF INVENTION: PLANTS
/ NUMBER OF SEQUENCES: 7
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D. C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-3518
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/204,288
/ FILING DATE: 10-MAR-1994
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9119279.9
/ FILING DATE: 10-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB92/01460
/ FILING DATE: 09-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KOKULIS, Paul N.
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: 206860/SBB36543/UST
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 861-3000
/ TELEFAX: (202) 822-0944
/ TELEX: 6714627 CUSH
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
```

LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-288-5

Query Match 78.3%; Score 1499.5; DB 1; Length 364;
Best Local Similarity 77.8%; Pred. No. 3.9e-158;
Matches 281; Conservative 36; Mismatches 41; Indels 3; Gaps 2;

QY 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 60
DB 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 58
QY 61 TSDIASKLPTKQPDAAVMDRLRLASYSVLTCSLRTLPGDKIERLYGLAPVCKELTGN 120
DB 59 PSLAAQLSTQNPDAVMDRLRLASYSVLTCSLRTLPGDKIERLYGLAPVCKELTGN 118
QY 121 DGVSIALLSLNNQKVLMSWYHLTEAVLEGIPFNKAYGNTAFEGTDPRENTVFN 180
DB 119 AGVSVAPLLNMQDKVLMSWYHLTEAVLEGIPFNKAYGNTAFEGTDPRENTVFN 178
QY 181 GMSNSTITMKKILETYGFBGLSVVDVGGTGTAHLNMTIAKYPMIKGINFDLPVLEE 240
DB 179 GMSNSTITMKKILETYGFBGLSVVDVGGTGTAHLNMTIAKYPMIKGINFDLPVLEE 238
QY 241 APSYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKKCYEALPTNGKYLAE 300
DB 239 APTYGVEHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKKCYEALPTNGKYLAE 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLAINPGGERKTEKFEALAKAGFEGF-RVAVSCAYNT 359
DB 299 ILPVAPDASLPTKAVVHIDVIMLAINPGGERKTEKFEALAKAGFEGF-RVAVSCAYNT 358
QY 360 W 360
DB 359 W 359

RESULT 8
US-09-500-569-18
Sequence 18, Application US/09500569
Patent No. 6329204
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafaleki, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REFERENCE: B1327 US NA
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 60/119,587
EARLIER FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 358
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: UNSURE
LOCATION: (134)
US-09-500-569-18

Query Match 77.9%; Score 1492; DB 2; Length 358;
Best Local Similarity 78.1%; Pred. No. 2.6e-157;
Matches 282; Conservative 39; Mismatches 36; Indels 4; Gaps 3;
QY 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 60
DB 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 58

QY 61 TSDIASKLPTKQPDAAVMDRLRLASYSVLTCSLRTLPGDKIERLYGL 120
DB 59 PSLAAQLSTQNPDAVMDRLRLASYSVLTCSLRTLPGDKIERLYGL 118
QY 121 DGVSIALLSLNNQKVLMSWYHLTEAVLEGIPFNKAYGNTAFEGT 180
DB 119 AGVSVAPLLNMQDKVLMSWYHLTEAVLEGIPFNKAYGNTAFEGT 178
QY 181 GMSNSTITMKKILETYGFBGLSVVDVGGTGTAHLNMTIAKYPMIKGINFDLPVLEE 240
DB 179 GMSNSTITMKKILETYGFBGLSVVDVGGTGTAHLNMTIAKYPMIKGINFDLPVLEE 238
QY 241 APSYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKKCYEALPTNGKYLAE 300
DB 239 APTYGVEHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKKCYEALPTNGKYLAE 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLAINPGGERKTEKFEALAKAGFEGF-RVAVSCAYNT 359
DB 299 ILPVAPDASLPTKAVVHIDVIMLAINPGGERKTEKFEALAKAGFEGF-RVAVSCAYNT 358
QY 360 W 360
DB 358 Y 358

RESULT 9
US-09-971-823B-18
Sequence 18, Application US/09971823B
Patent No. 6610521
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase
FILE REFERENCE: B1327 US NA
CURRENT APPLICATION NUMBER: US/09/971,823B
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/119,587
PRIOR FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 358
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: UNSURE
LOCATION: (134)
OTHER INFORMATION: Xaa = ANY AMINO ACID
US-09-971-823B-18

Query Match 77.9%; Score 1492; DB 2; Length 358
Best Local Similarity 78.1%; Pred. No. 2.6e-157;
Matches 282; Conservative 39; Mismatches 36; Indels 4; Gaps 3;
QY 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 60
DB 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 58
QY 61 TSDIASKLPTKQPDAAVMDRLRLASYSVLTCSLRTLPGDKIERLYGL 120
DB 59 PSLAAQLSTQNPDAVMDRLRLASYSVLTCSLRTLPGDKIERLYGL 118
QY 121 DGVSIALLSLNNQKVLMSWYHLTEAVLEGIPFNKAYGNTAFEGT 180
DB 119 AGVSVAPLLNMQDKVLMSWYHLTEAVLEGIPFNKAYGNTAFEGT 178
QY 181 GMSNSTITMKKILETYGFBGLSVVDVGGTGTAHLNMTIAKYPMIKGINFDLPVLEE 240
DB 179 GMSNSTITMKKILETYGFBGLSVVDVGGTGTAHLNMTIAKYPMIKGINFDLPVLEE 238
QY 241 APSYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKKCYEALPTNGKYLAE 300
DB 239 APTYGVEHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKKCYEALPTNGKYLAE 298

QY 318 IDVIMLANHPGKERTKEFEALAKGAGPEGRVVASCAVNTWITIEFLKX 367
DB 317 LDCHTLVHNGGSKERSKEDFEALASKTGSTVDVIC-CAYDTWVWELTKK 365

RESULT 15
US-08-204-288-7
Sequence 7, Application US/08204288
Patent No. 5959178
GENERAL INFORMATION:
APPLICANT: VAN DOORSSELAERE, Jan
APPLICANT: FRITTEG, Bernard J. M.
APPLICANT: INZE, Dirk G.
APPLICANT: JOUNANIN, Lise
APPLICANT: KNIGHT, Mary E.
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-288-7

Query Match 54.6%; Score 1045.5; DB 1; Length 365;
Best Local Similarity 57.1%; Pred. No. 1.6e-107;
Matches 210; Conservative 51; Mismatches 96; Indels 11; Gaps 7;

QY 5 SETKSPSEAAAAEEFAVFAMQLTSASVLPWVLSAIBLDVLEIMAKAGPGAHIISTSDI 64
DB 3 SSTK-SQIPTQSEEBENCTYAMQQLTSSSYLPFVLHSTIQLEVFELIAKSN-DTKLSASQI 60
QY 65 ASKLPF-KNPDAVMDRLRLASYSVLTCSLRTLPD----GKIBRLGLAPVCKFLTR 119
DB 61 VSOIPVCKNPDAATMDRLVYLASYSLFTCSI--VEDEENNGGQQRVYGLSQVGKFFVR 118
QY 120 NDDGVSIASIMNQKVLMEGSWYHLTEAVLEGIPFNKAYGWT-AFEYHGTDPRENTVF 178

DB 119 DEDGASWGPILLALLQDKVFINSWFEFKDAVLEGGVFPDRVHGVAFAFEYPI 178
QY 179 NNGMSNHSITIMKILLETYKGFEGIGSVVDVGGGIGALINMIIAKYPNIK 238
DB 179 NKAMINHTTVMKILLENYKGFENIKTLVDVGGGIGVNLKMITSKYPTIK 238
QY 239 EAPSPGVENHVGDMFVSPKGDALFMKWI CHDWSDEHCLKFLKCYEAL 298
DB 239 QHAPSPGVENHVGDMFVSPKGDALFMKWI LHODWSDEHCLKFLKCYEAL 298
QY 299 ECILPVADPDSLPTKAVVHIDVIMLANHPGKERTKEFEALAKGAGFEGI 358
DB 299 EALIPVKPDIDTAVVGVSQCDLIMMAQNPGGKERSSEEFALATEAGFKGI 357
QY 359 TWIIEFLK 366
DB 358 PWMEFCK 365

Search completed: December 12, 2005, 08:48:28
Job time : 48 secs